

volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent CC polymucleotide and amino acid sequences used in the exemplification of CC the present invention.

| | |
|-----------------|--|
| CC | antigenic epitopes or domains of prostate specific proteins |
| CC | polymucleotide and amino acid sequences used in the exemplification of CC the present invention |
| XX | Sequence 20 AA; |
| SQ | Query Match 100.0%; Score 100; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 1.3e-09; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 LLVVPAIKDKYGSQEDFTQV 20 |
| Db | 1 LLVVPAIKDKYGSQEDFTQV 20 |
| RESULT 3 | |
| CC | AAG99057 standard; peptide; 20 AA. |
| XX | Sequence 20 AA; |
| SQ | Query Match 100.0%; Score 100; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 1.3e-09; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 LLVVPAIKDKYGSQEDFTQV 20 |
| Db | 1 LLVVPAIKDKYGSQEDFTQV 20 |
| RESULT 4 | |
| CC | AAG99057 standard; peptide; 20 AA. |
| XX | Sequence 20 AA; |
| AC | AAG99057; |
| XX | DT 25-SEP-2001 (first entry) |
| XX | DE Human prostate-specific epitope mapping peptide #29. |
| XX | XX |
| XX | XX |
| DE | Human prostate cancer; therapy; cat eye syndrome; |
| XX | chromosome 22q11.2; prostate-specific protein; chromosome 1; |
| KW | prostate specific antigen; PSA. |
| KW | XX |
| OS | Homo sapiens. |
| OS | XX |
| PN | WO200134802-A2. |
| PN | XX |
| PD | 17-MAY-2001. |
| PD | XX |
| PD | 09-NOV-2000; 2000WO-US033904. |
| PF | XX |
| PF | PR 12-NOV-1999; |
| PF | 99US-00439313. |
| XX | PR 18-NOV-1999; |
| XX | 99US-00443686. |
| PA | (CORI-) CORIXA CORP. |
| XX | Xu J, Dillon DC, Mitcham JL, Harlocker SJ, Jiang Y, Reed SG, |
| PI | Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A; |
| PI | XX |
| XX | WPI; 2001-308785/32. |
| XX | Isolated polypeptide comprising at least an immunogenic portion of a PT prostate-specific protein, useful in the diagnosis and therapy of PT prostate cancer. |
| XX | XX |
| PS | Claim 3; Page 303; 325pp; English. |
| XX | The present invention describes an isolated polypeptide (P1) comprising CC at least an immunogenic portion of a prostate-specific protein, or its CC variant. Also described are polynucleotides (N1) encoding (P1) and CC (N1) have cytostatic activity and can be used in vaccine production. The CC present invention are polypeptides, nucleic acids and antibodies from the present invention are CC useful in the diagnosis and therapy of prostate cancer. Prostate specific CC genes P704P, P711P, P775P and B305D are located in a genomic CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region. CC Prostate specific antigen (PSA) P501S was located on chromosome 1. CC AAH84671 to AAH85143 and AAH99000 to AAG99077 represent Polynucleotide CC and polypeptide sequences used in the exemplification of the present CC invention |
| XX | XX |
| XX | Sequence 20 AA; |
| CC | Query Match 100.0%; Score 100; DB 4; Length 20; |
| CC | Best Local Similarity 100.0%; Pred. No. 1.3e-09; |
| CC | Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 LLVVPAIKDKYGSQEDFTQV 20 |
| Db | 1 LLVVPAIKDKYGSQEDFTQV 20 |

RESULT 4

ID ABU71708 standard; peptide; 20 AA.

XX AC ABU71708;

XX DT 10-JUN-2003 (first entry)

XX DE Prostate cancer therapy associated peptide #30.

XX KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen; PSMA.

XX OS Homo sapiens.

XX PN US2002192763-A1.

XX PD 19-DEC-2002.

XX PP 29-JUN-2001; 2001US-00895793.

XX PR 04-OCT-1999; 99US-0157455P.

PR 04-OCT-2000; 2000US-00679227.

PR 28-MAR-2001; 2001US-00822827.

XX PA (XUUJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L..

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CAPT/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A.

PA (HUBA/) HUBAL J.

PA (MCNE/) MCNEILL P D.

PA (HOUG/) HOUGHTON R L.

PA (DBAS/) Y DE BASSOLS C V.

PA (FORT/) FOX T M.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SJ, Jiang Y, Kalos MD, Carter D, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hurlal J, Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;

XX DR WPI: 2001-2450522.

XX PT Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.

XX PS Example 18; SEQ ID NO 522; 85pp; English.

CC The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or % sequence identity to any one of the 35 sequences defined in the USPRO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This is the amino acid sequence of a

CC prostate cancer therapy associated peptide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US Patent Office at seqdata.uspto.gov/sequence.html?DocID=US20020192763

CC SQ Sequence 20 AA;

Query Match 100.0%; Score 100; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.3e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 LLVVAIKKDYGQSQEDFTQV 20
| | | | | | | | | | | | | | | |
1 LLVVAIKKDYGQSQEDFTQV 20

Db

RESULT 5

ABB95277

ID ABB95277 standard; peptide; 20 AA.

XX AC ABB95277;

XX DT 19-JUL-2002 (first entry)

XX DE Epitope mapping study peptide SEQ ID NO 522.

XX KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; gene therapy.

XX OS Unidentified.

XX PN US200202248-A1.

XX PD 21-FEB-2002.

XX PF 12-JAN-2001; 2001US-00759143.

XX PR 25-FEB-1997; 97US-0086099.

PR 01-AUG-1997; 97US-0094804.

PR 10-FEB-1998; 98US-0000956.

PR 25-FEB-1998; 98US-0000607.

PR 14-JUL-1998; 98US-00115453.

PR 23-SEP-1998; 98US-00115812.

PR 15-JAN-1999; 99US-0022149.

PR 09-APR-1999; 99US-00288946.

PR 13-JUL-1999; 99US-0032616.

PR 12-NOV-1999; 99US-0049313.

PR 18-NOV-1999; 99US-00443686.

PR 14-JAN-2000; 2000US-00433672.

PR 27-MAR-2000; 2000US-00556857.

PR 09-MAY-2000; 2000US-0058100.

PR 12-MAY-2000; 2000US-0050737.

PR 13-JUN-2000; 2000US-0053793.

PR 27-JUN-2000; 2000US-0065783.

PR 10-AUG-2000; 2000US-00616215.

PR 29-AUG-2000; 2000US-00651236.

PR 06-SEP-2000; 2000US-00651236.

PR 02-OCT-2000; 2000US-00679426.

PR 10-OCT-2000; 2000US-00665166.

XX PA (XUUJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.
 PA (SKEIKY/) SKEIKY Y A W.
 PA (HEPLER/) HEPLER W T.
 PA (HENDRICKSON/) HENDERSON R A.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocke SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedick TS,
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX
 DR WPI: 2002-255649/30.
 PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer.
 XX
 PS Claim 2; SEQ ID NO 522; 87pp; English.
 XX
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancer, particularly prostate cancer. The present sequence is a
 CC peptide described in the invention
 XX
 Sequence 20 AA;
 PT Query Match 100.0%; Score 100; DB 5; Length 20;
 PT Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 PT Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT DT 18-DEC-2003 (first entry)
 PT XX
 DE Human prostate protein P503S epitope mapping peptide #2099.
 DE XX
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
 KW cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell; epitope.
 XX
 ID ABR54389 standard; protein; 20 AA.
 OS Homo sapiens.
 XX
 AC ABR54389;
 PN US2003185830-A1.
 XX
 DT 28-AUG-2003 (first entry)
 XX
 DE Prostate tumour specific related peptide for epitope mapping SEQ ID 522.
 XX
 KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
 KW immune response; prostate cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2002B8747-A2.
 XX
 PD 14-NOV-2002.
 XX
 09-MAY-2002; 2002WO-US014753.
 XX
 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 PA (CORIXA CORP.
 XX
 Xu J, Dillon DC, Mitcham JL, Harlocke SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedick TS;
 Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 McNeill PD, Houghton RL, Vinals Y De Bassols, Foy TM, Watanabe Y;
 PI Deng T;
 XX
 DR WPI; 2003-167130/16.
 XX
 New prostate-specific proteins and genes, useful in gene therapy,
 PT particularly for stimulating an immune response in a patient, or treating
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 XX

PS Example 18; Page 470-471; 691pp; English.
 XX
 CC The present invention relates to novel prostate-specific proteins (PSP)
 CC and their coding sequences. The PSPs and their coding sequences are
 CC useful for stimulating an immune response in a patient, or for treating
 CC prostate cancer in a patient and for determining, detecting or diagnosing
 CC the presence of a cancer in a patient. The present sequence was used to
 CC illustrate the invention
 XX
 SQ Sequence 20 AA;
 PT Query Match 100.0%; Score 100; DB 6; Length 20;
 PT Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 PT Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT DT 18-DEC-2003 (first entry)
 PT XX
 DE Human prostate protein P503S epitope mapping peptide #2099.
 DE XX
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
 KW cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell; epitope.
 XX
 ID ADB13972 standard; peptide; 20 AA.
 ID ADB13972
 AC ADB13972;
 XX
 DT 18-DEC-2003 (first entry)
 PT XX
 DE Human prostate protein P503S epitope mapping peptide #2099.
 DE XX
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
 KW cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell; epitope.
 XX
 OS Homo sapiens.
 XX
 PN US2003185830-A1.
 XX
 DT 02-OCT-2003.
 XX
 DE 02-NOV-2002; 2002US-00294025.
 DE XX
 PR 25-FEB-1997; 97US-00805099.
 PR 01-AUG-1997; 97US-0090804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00158812.
 PR 15-JAN-1999; 99US-0023149.
 PR 09-APR-1999; 99US-0028946.
 PR 13-JUL-1999; 99US-0035616.
 PR 12-NOV-1999; 99US-0043313.
 PR 18-NOV-1999; 99US-0044686.
 PR 14-JAN-2000; 2000US-00481672.
 PR 27-MAR-2000; 2000US-0538857.
 PR 09-MAY-2000; 2000US-0056100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-0597793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-0652336.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-00670426.
 PR 10-OCT-2000; 2000US-0685166.
 PR 09-NOV-2000; 2000US-0701629.
 PR 12-JAN-2001; 2001US-0075143.
 PR 09-FEB-2001; 2001US-0078669.
 PR 09-MAY-2001; 2001US-0085911.
 PR 10-DEC-2001; 2001US-00012896.
 PR 09-MAY-2002; 2002US-00144678.
 XX

PA (CORI-X) CORIXA CORP.
 XX
 PI Xu J, Stolk JA, Kalos MD;
 XX DR WPI: 2003-756193/71.
 XX PT New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate cancer.
 PT
 XX PS Example 18; Page; 101pp; English.
 XX
 The invention relates to an isolated polypeptide comprising no more than 11-512 amino acids of ADB13563 comprising a sequence of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific cDNA, one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the peptides or a polypeptide appearing as ADB1355), detecting the amount of polypeptide that binds to the agent and comparing the amount of polypeptide to a predetermined cut-off value to determine the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the peptides or the isolated T cell population, treating prostate cancer in a patient comprising administering a composition comprising the peptides, nucleic acids, antibodies or compounds, determining the presence of a cancer in a patient and treating prostate cancer in a patient comprising incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated from a patient with the peptides or antigen presenting cells that express the peptides so that the T cells proliferate, and administering the proliferated T cells to the patient. The peptides (or an oligonucleotide that hybridises to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides, nucleic acids encoding, or antigen-presenting cells expressing the nucleic acid, are used to stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is an epitope or peptide derived from one of the prostate specific proteins of the invention. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.
 XX Sequence 20 AA;
 XX Query Match Score 100%; Score 100%; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 Qy 1 LLVVPAIKDKYGSQEDFTQV 20
 Db 1 LLVVPAIKDKYGSQEDFTQV 20
 RESULT 8
 ADG26388 standard; peptide; 20 AA.
 ID ADG26388
 AC ADG26388;
 XX DT 26-PBB-2004 (first entry)
 XX Human prostate-specific polypeptide #58.
 XX Homo sapiens.
 XX Query Match 100.0%; Score 100%; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB Human secreted polypeptide #150.
 XX Human; secreted protein; genetic disease.
 XX OS Homo sapiens.
 XX PN US2004110939-A1.
 XX PD 10-JUN-2004.
 XX PP 15-OCT-2001; 2001US-00978360.
 XX PR 17-DEC-1998; 98WO-JB002122.
 PR 09-FEB-1999; 99WO-JB00022.
 PR 21-JUN-2000; 2000WO-JB000951.
 PR 15-SEP-2000; 2000US-00663600.
 XX PA (GEST) GENSET SA.
 XX PI Dumas Milne Edwards J, Bougueret L, Jobert S, Cluseel C;
 PI Duclerc A;
 XX WPI; 2004-440404/41.
 DR N-PSDB; ADP18894.
 DR XX PT New isolated polynucleotide encoding secreted polypeptide, useful for gene therapy, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes.
 XX PS Claim 2; SEQ ID NO 555; 113pp; English.
 XX CC The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polynucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing human tissues and cells from non-human tissues and cells, and for distinguishing between human tissues and cells that do not express the polynucleotides comprising the cDNAs. The polynucleotides and polypeptides are useful in forensic procedures or diagnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence represents a human secreted polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
 XX SQ Sequence 126 AA;
 XX Query Match 100.0%; Score 100; DB 8; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLVVPAIKKDYGQSQEDFTQV 20
 Db 70 LLVVPAIKKDYGQSQEDFTQV 89
 RESULT 12
 ADD65950 ID ADD65950 standard; protein; 172 AA.
 XX AC ADD65950;
 XX DT 15-JAN-2004 (first entry)
 DE Human REMAP protein - SEQ ID 19.
 XX KW human; receptor and membrane-associated protein; REMAP; cytostatic; anti-arteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thymomimetic; cell proliferative; cancer; atherosclerosis; neurological; metastatic; cancer; vaccine; cytotoxic; human; normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA; KW metstatic; cancer; vaccine; cytotoxic; human.

KW epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS; allergy; developmental; hypothyroidism; Cushing's syndrome; infection.
 XX OS Homo sapiens.
 XX PN WO2003048305-A2.
 XX PD 12-JUN-2003.
 XX PP 13-NOV-2002; 2002WO-US036759.
 XX PR 13-NOV-2001; 2001US-0333097P.
 PR 15-NOV-2001; 2001US-0333274P.
 PR 14-DEC-2001; 2001US-0340542P.
 PR 18-DIC-2001; 2001US-034166P.
 PR 11-JAN-2002; 2002US-0341580P.
 PR 14-JAN-2002; 2002US-0348687P.
 XX PA (INCYT-) INCYTE GENOMICS INC.
 XX PI Dugyan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y;
 PI Chawla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehr-Mason PM;
 PI Thangavelu K, Lee S, Emerling BM, Kable AE, Baughn MR;
 PI Gandhi AR, Tran UK, Richardson TW, Marquis JP, Lal PG, Foraythe IJ;
 PI Lee EA, Swarrikar A, Hallick JA, Griffin JA, Elliott VS, Gorvad AB;
 PI Hafalia AJA, Ison CH, Jin P, Jiang X, Bhatia AA,
 PI Burrill JD, Blake JJ, Ho A, Zhang W, Gao J;
 XX DR WPI; 2003-513744/48.
 XX DR N-PSDB; ADP69337.
 XX PT New human receptors and membrane-associated proteins (REMAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or infections.
 XX PS Claim 1; SEQ ID NO 19; 298pp; English.
 XX PT The invention relates to a novel isolated polypeptide comprising a human receptor and membrane-associated protein (REMAP). The polypeptide of the invention demonstrates cytotatic, antiarteriosclerotic, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic, antinflammatory and thymomimetic activities and may be useful for treating and diagnosing various disorders including those which are cell proliferative such as cancer and atherosclerosis, neurological including epilepsy, Huntington's disease and stroke, immune/inflammatory particularly AIDS and allergies and developmental such as hypothyroidism and Cushing's syndrome, as well as infections. The current sequence is that of the human REMAP protein of the invention.
 XX SQ Sequence 172 AA;
 XX Query Match 100.0%; Score 100; DB 7; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLVVPAIKKDYGQSQEDFTQV 20
 Db 51 LLVVPAIKKDYGQSQEDFTQV 70
 RESULT 13
 ADD65950 ID ADD65950 standard; protein; 174 AA.
 XX AC ADD65950;
 XX DT 09-SEP-2004 (first entry)
 DE Protein of human ovarian specific gene, SEQ ID No 157.
 XX KW human; receptor and membrane-associated protein; REMAP; cytostatic; anti-arteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thymomimetic; cell proliferative; cancer; atherosclerosis; neurological; metastatic; cancer; vaccine; cytotoxic; human.

Db 93 LLVVPATKKDYGQSQEDFTQV 112

RESULT 15

ID ADR66892 standard; protein; 214 AA.

XX AC ADR66892;

XX XX Human prostatic carcinoma derived DNA SEQ ID 190 #4.

KW human; cytosstatic; diagnosis; prostatic cancer; differential expression analysis.

KW Homo sapiens.

OS XX WO2004076614-A2.

PN XX PD 10-SEP-2004.

PP XX 22-FEB-2004; 2004WO-DE0000433.

PR XX 27-FEB-2003; 2003DE-01009985.

PR PR 14-MAY-2003; 2003DE-01022134.

XX PA (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.

PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.

PA (PILA/) PILARSKY C.

XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;

PI Schmitt A, Beckmann G, Bruemmendorf T, Kinnemann H, Roedcke S;

PI Xinzhang L, Straub B;

XX DR WPI; 2004-653386/63.

XX PT New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding agents.

XX PS Claim 2; Page 1545; 1607pp; German.

XX This invention describes novel cytosstatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the

CC polynucleotide and polypeptide sequences used in the method of the invention.

CC

XX Sequence 214 AA;

SQ Query Match 100.0%; Score 100; DB 8; Length 214;

CC Best Local Similarity 100.0%; Pred. No. 2e-08;

CC Matches 20; Conservative 0; Mismatches 0;

CC Indels 0; Gaps 0;

QY 1 LLVVPATKKDYGQSQEDFTQV 20

DB 93 LLVVPATKKDYGQSQEDFTQV 112

Search completed: February 5, 2005, 19:59:54

Job time : 107.746 secs

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| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------------------|---------------------|
| 1 | 100 | 100.0 | 20 | 3 US-09-439-313-522 | Sequence 522, App |
| 2 | 100 | 100.0 | 20 | 4 US-09-436-215-522 | Sequence 522, App |
| 3 | 100 | 100.0 | 20 | 4 US-09-685-166A-522 | Sequence 522, App |
| 4 | 100 | 100.0 | 20 | 4 US-09-426-522 | Sequence 522, App |
| 5 | 100 | 100.0 | 20 | 4 US-09-159-143-522 | Sequence 522, App |
| 6 | 100 | 100.0 | 20 | 4 US-09-051-336-522 | Sequence 522, App |
| 7 | 100 | 100.0 | 233 | 4 US-09-145-515-137 | Sequence 137, App |
| 8 | 100 | 100.0 | 241 | 3 US-08-108-148-1 | Sequence 1, Appli |
| 9 | 100 | 100.0 | 241 | 3 US-09-020-956-114 | Sequence 114, App |
| 10 | 100 | 100.0 | 241 | 3 US-09-030-607-114 | Sequence 114, App |
| 11 | 100 | 100.0 | 241 | 3 US-09-339-313-114 | Sequence 114, App |
| 12 | 100 | 100.0 | 241 | 3 US-09-352-616A-114 | Sequence 114, App |
| 13 | 100 | 100.0 | 241 | 4 US-09-232-149A-114 | Sequence 114, App |
| 14 | 100 | 100.0 | 241 | 4 US-09-159-912-114 | Sequence 114, App |
| 15 | 100 | 100.0 | 241 | 4 US-09-636-215-114 | Sequence 114, App |
| 16 | 100 | 100.0 | 241 | 4 US-09-685-166A-114 | Sequence 114, App |
| 17 | 100 | 100.0 | 241 | 4 US-09-115-153-114 | Sequence 114, App |
| 18 | 100 | 100.0 | 241 | 4 US-09-688-189-114 | Sequence 114, App |
| 19 | 100 | 100.0 | 241 | 4 US-09-426-114 | Sequence 114, App |
| 20 | 100 | 100.0 | 241 | 4 US-09-579-143-114 | Sequence 114, App |
| 21 | 100 | 100.0 | 241 | 4 US-09-551-336-114 | Sequence 114, App |
| 22 | 47 | 47.0 | 93 | 4 US-09-543-661A-678/7 | Sequence 678/7, App |
| 23 | 45 | 45.0 | 162 | 4 US-09-589-039A-10419 | Sequence 10419, A |
| 24 | 43.5 | 43.5 | 272 | 4 US-09-583-110-4023 | Sequence 4023, Ap |
| 25 | 43.5 | 43.5 | 277 | 4 US-09-333-3350 | Sequence 3350, Ap |
| 26 | 43 | 43.0 | 155 | 4 US-09-543-581A-7489 | Sequence 7489, Ap |
| 27 | 43 | 43.0 | 159 | 4 US-09-540-236-1985 | Sequence 1985, Ap |

RESULT 4
 US-09-679-426-522
 Query Match 100.0%; Score 100; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 522 Application US/09679426
 Qy 1 LLVVPATKKDYGSGQEDFTQV 20
 Db 1 LLVVPATKKDYGSGQEDFTQV 20

RESULT 4
 US-09-679-426-522
 Sequence 522, Application US/09679426
 Patent No. 6759515
 GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun C.
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yuqui
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Fanger, Gary R.
 / APPLICANT: Rettler, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Li, Samuel
 / APPLICANT: Wang, Ajjun
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Hepler, William
 / APPLICANT: Repler, William
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 / DIAGNOSIS OF PROSTATE CANCER
 / FILE REFERENCE: 210121.4271C17
 / CURRENT APPLICATION NUMBER: US/09/636,215
 / CURRENT FILING DATE: 2000-08-10
 / NUMBER OF SEQ ID NOS: 852
 / SOFTWARE: FastSEQ For Windows Version 3.0
 / SEQ ID NO: 522
 / LENGTH: 20
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Made in a lab
 US-09-636-215-522

Query Match 100.0%; Score 100; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 522 Application US/09636215
 Qy 1 LLVVPATKKDYGSGQEDFTQV 20
 Db 1 LLVVPATKKDYGSGQEDFTQV 20

RESULT 3
 US-09-685-166A-522
 Patent No. 6630305
 GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun C.
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yuqui
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Fanger, Gary R.
 / APPLICANT: Rettler, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Li, Samuel
 / APPLICANT: Wang, Ajjun
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Hepler, William
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 / DIAGNOSIS OF PROSTATE CANCER
 / FILE REFERENCE: 210121.427C21
 / CURRENT APPLICATION NUMBER: US/09/685,166A
 / CURRENT FILING DATE: 2000-10-10
 / NUMBER OF SEQ ID NOS: 88
 / SOFTWARE: FastSEQ For Windows Version 3.0
 / SEQ ID NO: 522
 / LENGTH: 20
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Made in a lab
 US-09-685-166A-522

RESULT 5
 US-09-759-143-522
 Sequence 522, Application US/09759143
 Patent No. 6800746
 GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun C.
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Fanger, Gary R.
 / APPLICANT: Rettler, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.427023
 CURRENT APPLICATION NUMBER: US/09/759,143
 CURRENT FILING DATE: 2001-01-12
 NUMBER OF SEQ ID NOS: 934
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 522
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Made in a lab

Query Match 100.0%; Score 100; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | |
|----|--------------------------|
| Qy | 1 LLVVPALKDYGQSQEDTQV 20 |
| Db | 1 LLVVPALKDYGQSQEDTQV 20 |

RESULT 6
 US-09-651-236-522
 Sequence 522, Application US/09651236
 Parent No. 6818751
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Derrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.42718C18
 CURRENT APPLICATION NUMBER: US/09/651,236
 CURRENT FILING DATE: 2000-08-29
 NUMBER OF SEQ ID NOS: 865
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 522
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Made in a lab

Query Match 100.0%; Score 100; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | |
|----|--------------------------|
| Qy | 1 LLVVPALKDYGQSQEDTQV 20 |
| Db | 1 LLVVPALKDYGQSQEDTQV 20 |

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; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER APPLICATION NUMBER: 60/043,568 ; EARLIER FILING DATE: 05-Sep-1997
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER APPLICATION NUMBER: 60/043,314 ; EARLIER FILING DATE: 1997-05-23
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER APPLICATION NUMBER: 60/043,569 ; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,311 ; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-04-11 ; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,671 ; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER APPLICATION NUMBER: 60/043,674 ; EARLIER FILING DATE: 1997-05-23
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER APPLICATION NUMBER: 60/043,672 ; EARLIER FILING DATE: 1997-05-23
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER APPLICATION NUMBER: 60/043,669 ; EARLIER FILING DATE: 1997-05-23
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER APPLICATION NUMBER: 60/043,312 ; EARLIER FILING DATE: 1997-05-23
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER APPLICATION NUMBER: 60/043,313 ; EARLIER FILING DATE: 1997-05-23
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER APPLICATION NUMBER: 60/043,672 ; EARLIER FILING DATE: 1997-05-23
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER APPLICATION NUMBER: 60/043,315 ; EARLIER FILING DATE: 1997-04-11
; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER APPLICATION NUMBER: 60/048,974 ; EARLIER FILING DATE: 1997-04-11
; EARLIER FILING DATE: 1997-06-06 ; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER APPLICATION NUMBER: 60/056,886 ; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/056,877 ; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-08-22 ; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,889 ; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22 ; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893 ; EARLIER APPLICATION NUMBER: 60/056,644
; EARLIER FILING DATE: 1997-08-22 ; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630 ; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22 ; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878 ; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22 ; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662 ; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER APPLICATION NUMBER: 60/056,637 ; EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER APPLICATION NUMBER: 60/056,882 ; EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER APPLICATION NUMBER: 60/056,637 ; EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER APPLICATION NUMBER: 60/056,903 ; EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER APPLICATION NUMBER: 60/056,888 ; EARLIER FILING DATE: 1997-06-06
; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/057,655
; EARLIER APPLICATION NUMBER: 60/056,879 ; EARLIER FILING DATE: 1997-09-05
; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER APPLICATION NUMBER: 60/056,880 ; EARLIER FILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-08-22 ; NUMBER OF SEQ ID NOS: 280
; EARLIER APPLICATION NUMBER: 60/056,894 ; SOFTWARE: PatentIn Ver. 2.0
; EARLIER FILING DATE: 1997-08-22 ; SEQ ID NO: 137
; LENGTH: 233 ; LENGTH: 233;
; Query Match 100.0%; Score 100; DB 4;
; Best Local Similarity 100.0%; Pred. No. 5.7e-10;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKKDYGSQEDFTQV 20
Db 111 LLVVPAIKKDYGSQEDFTQV 130

RESULT 8
US-08-008-148-1
; Sequence 1, Application US/08808148
; Patent No. 6030478
; GENERAL INFORMATION:
; APPLICANT: Hiliman, Jennifer
;
```

APPLICANT: Goli, Surya
 APPLICANT: Zhang, Hong Wolfe
 TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/808,148
 FILING DATE: Herewith
 REFERENCE/DOCKET NUMBER: PR-0218 US
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE: PROSNOT26
 LIBRARY: PROSNOT26
 CLONE: 2187263

US-08-808-148-1
 Query Match 100.0%; Score 100; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 LLVVPAIKDKYGSQEDFTQV 20
 Db 120 LLVVPAIKDKYGSQEDFTQV 139

RESULT 9
 US-09-020-956-114
 Sequence 114, Application US/09020956
 Patent No. 6261562
 GENERAL INFORMATION:
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 NUMBER OF SEQUENCES: 178
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 US-09-020-956-114
 Sequence 114, Application US/09020956
 Patent No. 6261562
 GENERAL INFORMATION:
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 NUMBER OF SEQUENCES: 178
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/020,956
 FILING DATE: 09-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121,427C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6311
 INFORMATION FOR SEQ ID NO: 114:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-020-956-114

Query Match 100.0%; Score 100; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDKYGSQEDFTQV 20
 Db 120 LLVVPAIKDKYGSQEDFTQV 139

RESULT 10
 US-09-030-607-114
 Sequence 114, Application US/09030607
 Patent No. 6262245
 GENERAL INFORMATION:
 APPLICANT: XU, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 US-09-030-607-114
 Sequence 114, Application US/09030607
 Patent No. 6262245
 GENERAL INFORMATION:
 APPLICANT: XU, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

Query Match 100.0%; Score 100; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 6e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVYPAIKKDYGSGQEDFTQV 20
 Db 120 LLVYPAIKKDYGSGQEDFTQV 139

RESULT 13
 US-09-232-149A-114
 ; Sequence 114, Application US/09232149A
 ; Patent No. 6463611
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
 ; FILE REFERENCE: 210121-427C6
 ; CURRENT APPLICATION NUMBER: US/09/232,149A
 ; CURRENT FILING DATE: 1999-01-15
 ; NUMBER OF SEQ ID NOS: 338
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 114
 ; LENGTH: 241
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-232-149A-114

Query Match 100.0%; Score 100; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 6e-10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVYPAIKKDYGSGQEDFTQV 20
 Db 120 LLVYPAIKKDYGSGQEDFTQV 139

RESULT 14
 US-09-159-812-114
 ; Sequence 114, Application US/09159812A
 ; Patent No. 6613872
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
 ; FILE REFERENCE: 210121-428C5
 ; CURRENT APPLICATION NUMBER: US/09/159,812A
 ; CURRENT FILING DATE: 1998-09-23
 ; NUMBER OF SEQ ID NOS: 306
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 114
 ; LENGTH: 241
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-159-812-114

Query Match 100.0%; Score 100; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 6e-10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVYPAIKKDYGSGQEDFTQV 20
 Db 120 LLVYPAIKKDYGSGQEDFTQV 139

RESULT 15
 US-09-332-616A-114
 ; Sequence 114, Application US/09332616A
 ; Patent No. 6395378
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121-427C8
 ; CURRENT APPLICATION NUMBER: US/09/352,616A
 ; CURRENT FILING DATE: 1999-07-13
 ; NUMBER OF SEQ ID NOS: 472
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 114
 ; LENGTH: 241
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-332-616A-114

Query Match 100.0%; Score 100; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 6e-10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVYPAIKKDYGSGQEDFTQV 20
 Db 120 LLVYPAIKKDYGSGQEDFTQV 139

RESULT 15
 US-09-636-215-114
 ; Sequence 114, Application US/09636215
 ; Patent No. 6620922
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedwick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Ajun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Heppler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/635,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 114
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapien
US-09-636-215-114

Query Match 100 0%; Score 100; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLVVPAIKDKYGSQEDFTQV 20
Db 120 LLVVPAIKDKYGSQEDFTQV 139

Search completed: February 5, 2005; 20:07:12
Job time : 34.4237 secs

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Query Match 100.0%; Score 100; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 SEQ ID NO: 09-822-827-522

RESULT 2
 Query Match 100.0%; Score 100; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 US-09-780-669-522
 Sequence 522, Application US/09780669
 Patent No. US2002005197A1

GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqui
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedrick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William L.
 APPLICANT: Hurl, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 CURRENT APPLICATION NUMBER: US/09/780,669
 FILE REFERENCE: 210121-427C4
 CURRENT FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 943
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 522
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab
 US-09-780-669-522

Query Match 100.0%; Score 100; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 SEQ ID NO: 09-822-827-522
 Sequence 522, Application US/09822827
 Patent No. US20020081610A1

GENERAL INFORMATION:
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121-534C1
 CURRENT APPLICATION NUMBER: US/09/822,827
 CURRENT FILING DATE: 2001-03-28
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 522

RESULT 4
 Query Match 100.0%; Score 100; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 US-09-895-793-522
 Sequence 522, Application US/09895793
 Publication No. US20020192763A1

GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqui
 APPLICANT: Kalos, Michael D.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedrick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William L.
 APPLICANT: Hurl, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Vinala de Bassols, Carlota
 APPLICANT: Foy, Teresa
 APPLICANT: Fanger, Gary R.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121-534C2
 CURRENT APPLICATION NUMBER: US/09/895,793
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 522

Query Match 100.0%; Score 100; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 SEQ ID NO: 09-895-793-522
 Sequence 522, Application US/09895793
 Publication No. US20020192763A1

GENERAL INFORMATION:
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121-534C1
 CURRENT APPLICATION NUMBER: US/09/822,827
 CURRENT FILING DATE: 2001-03-28
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 522

RESULT 5
 Query Match 100.0%; Score 100; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 US-09-895-814-522
 Sequence 522, Application US/09895814
 Publication No. US2002013296A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yiqiu
 APPLICANT: Kalos, Michael D.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William T.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Hural, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Vinals de Bassols, Cariota
 APPLICANT: Foy, Teresa
 APPLICANT: Pancer, Gary R.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.427626
 CURRENT APPLICATION NUMBER: US/09/895, 814
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 990
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 522
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

US-09-895-814-522

Query Match 100.0%; Score 100; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDYGSQEDFTQV 20
 Db 1 LLVVPAIKDYGSQEDFTQV 20

RESULT 6
 US-10-012-896-522
 Sequence 522, Application US/10012896
 Publication No. US20020183251A1
 GENERAL INFORMATION:
 APPLICANT: Jiang, Yiqiu
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Vedick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William T.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Hural, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Vinals de Bassols, Cariota
 APPLICANT: Foy, Teresa
 APPLICANT: Pancer, Gary R.
 APPLICANT: Wantanabe, Yoshihiro

US-10-012-896-522

Query Match 100.0%; Score 100; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDYGSQEDFTQV 20
 Db 1 LLVVPAIKDYGSQEDFTQV 20

RESULT 7
 US-10-010-940-522
 Sequence 522, Application US/10010940
 Publication No. US20030088062A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan Louise
 APPLICANT: Jiang, Yugu
 APPLICANT: Reed, Steven G.
 APPLICANT: Kalos, Michael
 APPLICANT: Fanger, Gary
 APPLICANT: Retter, Mark
 APPLICANT: Solit, John
 APPLICANT: Day, Craig
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.427D3
 CURRENT APPLICATION NUMBER: US/010, 940
 NUMBER OF SEQ ID NOS: 575
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 522
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

US-10-010-940-522

Query Match 100.0%; Score 100; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDYGSQEDFTQV 20
 Db 1 LLVVPAIKDYGSQEDFTQV 20

RESULT 8
 US-10-144-678A-522
 Sequence 522, Application US/10144678A
 Publication No. US2003015789A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.

RESULT 10
 1 LLVVPAIKDKDGSQEDFTQV 20
 Db

RESULT 10
 US-09-978-160A-555
 ; Sequence 555, Application US/09978360A
 ; Publication No. US2004110939A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
 ; APPLICANT: Bouquerel, Lydie
 ; APPLICANT: Jobert, Severin
 ; APPLICANT: Clusei, Catherine
 ; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
 ; FILE REFERENCE: 56_USA.CIP
 ; CURRENT APPLICATION NUMBER: US/09/978-360A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: US 60/066,677
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: US 60/069,957
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: US 60/074,121
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: US 60/081,563
 ; PRIOR FILING DATE: 1998-04-13
 ; PRIOR APPLICATION NUMBER: US 60/096,116
 ; PRIOR FILING DATE: 1998-08-10
 ; PRIOR APPLICATION NUMBER: US 60/099,273
 ; PRIOR FILING DATE: -09-04
 ; PRIOR APPLICATION NUMBER: US 09/191,997
 ; PRIOR FILING DATE: 1998-11-13
 ; PRIOR APPLICATION NUMBER: US 09/215,435
 ; PRIOR FILING DATE: 1998-12-17
 ; PRIOR APPLICATION NUMBER: PCT/IB98/02122
 ; PRIOR FILING DATE: 1998-12-17
 ; PRIOR APPLICATION NUMBER: US 09/247,155
 ; PRIOR FILING DATE: 1999-02-09
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 810
 ; SEQ ID NO: 522
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 ; US-10-144-678A-522

Query Match Score 100; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDKDGSQEDFTQV 20
 Db 1 LLVVPAIKDKDGSQEDFTQV 20

RESULT 9
 US-10-294-025-522
 ; Sequence 522, Application US/10294025
 ; Publication No. US20030185830A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Xu, Jianchun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C29
 ; CURRENT APPLICATION NUMBER: US/10/294,025
 ; CURRENT FILING DATE: 2002-11-12
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 522
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 ; US-10-294-025-522

Query Match Score 100; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDKDGSQEDFTQV 20
 Db 70 LLVVPAIKDKDGSQEDFTQV 89

RESULT 11
 US-09-981-876-137
 ; Sequence 137, Application US/09981876
 ; Patent No. US20020164669A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 70 Human Secreted Proteins
 ; CURRENT APPLICATION NUMBER: US/09/981,876
 ; CURRENT FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US/09/981,876
 ; PRIOR FILING DATE: 1998-09-04
 ; PRIOR APPLICATION NUMBER: 60/040,162
 ; PRIOR FILING DATE: 1997-03-07

Query Match Score 100; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDKDGSQEDFTQV 20

PRIOR APPLICATION NUMBER: 60/047,589
 PRIOR FILING DATE: 1997-05-23
 PRIOR APPLICATION NUMBER: 60/047,593
 PRIOR FILING DATE: 1997-05-23
 PRIOR APPLICATION NUMBER: 60/047,614
 PRIOR FILING DATE: 1997-05-23
 PRIOR APPLICATION NUMBER: 60/043,578
 PRIOR FILING DATE: 1997-04-11
 PRIOR APPLICATION NUMBER: 60/043,576
 PRIOR FILING DATE: 1997-04-11
 PRIOR APPLICATION NUMBER: 60/047,501
 PRIOR FILING DATE: 1997-05-23
 PRIOR APPLICATION NUMBER: 60/043,670
 PRIOR FILING DATE: 1997-04-11
 PRIOR APPLICATION NUMBER: 60/056,881
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056,664
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056,876
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056,882
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056,909
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056,875
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056,862
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056,887
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056,908
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/048,964
 PRIOR FILING DATE: 1997-06-06
 PRIOR APPLICATION NUMBER: 60/057,650
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: 60/056,884
 PRIOR FILING DATE: 1997-08-22
 NUMBER OF SEQ ID NOS: 280
 SOFTWARE: PatentIn ver. 2.0
 SEQ ID NO: 137
 LENGTH: 233

Query Match 100.0%; Score 100; DB 9; Length 233;
 Best Local Similarity 100.0%; Pred. No. 9_6e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDKDYGSQEDFTQV 20
 Db 111 LLVVPAIKDKDYGSQEDFTQV 130

RESULT 12
 US-09-148-545-137
 ; Sequence 137, Application US/09148545
 ; FILE REFERENCE: P20101B1
 ; PUBLIC INFORMATION: US2010027132A1
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 70 Human Secreted Proteins
 ; CURRENT APPLICATION NUMBER: US/09/148,545
 ; CURRENT FILING DATE: 1998-09-04
 ; EARLIER APPLICATION NUMBER: PCT/US98/04482
 ; EARLIER FILING DATE: 1998-03-06
 ; EARLIER APPLICATION NUMBER: 60/040,162
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,333
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/038,621
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,161
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,626
 ; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,578

; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,981
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,962
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 137
; LENGTH: 233 ;
Query Match 100.0%; Score 100; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIORITY APPLICATION NUMBER: PCT/US01/16450
; PRIORITY FILING DATE: 2001-05-18
; PRIORITY APPLICATION NUMBER: US 10-264-237-1489
; PRIORITY FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 1489
; LENGTH: 240 ;
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-237-1489
Query Match 100.0%; Score 100; DB 15;
Best Local Similarity 100.0%; Pred. No. 9.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIORITY APPLICATION NUMBER: PCT/US01/16450
; PRIORITY FILING DATE: 2001-05-18
; PRIORITY APPLICATION NUMBER: US 10-264-237-1489
; PRIORITY FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 1489
; LENGTH: 240 ;
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-237-1489
Query Match 100.0%; Score 100; DB 15;
Best Local Similarity 100.0%; Pred. No. 9.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 119 LLVPAIKKDYGSOQEDFTQV 138

RESULT 14
US-09-759-143-114
Sequence 114, Application US/09759143
GENERAL INFORMATION:
| APPLICANT: Xu, Jiangchun
| APPLICANT: Dillon, Davin C.
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Harlocker, Susan L.
| APPLICANT: Jiang, Yuqui
| APPLICANT: Henderson, Robert A.
| APPLICANT: Kalos, Michael D.
| APPLICANT: Fanger, Gary R.
| APPLICANT: Retter, Marc W.
| APPLICANT: Stolk, John A.
| APPLICANT: Day, Craig H.
| APPLICANT: Vedwick, Thomas S.
| APPLICANT: Carter, Darrick
| APPLICANT: Li, Samuel
| APPLICANT: Wang, Ajun
| APPLICANT: Skeiky, Yasir A.W.
| APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER

| FILE REFERENCE: 210121..427C24
| CURRENT APPLICATION NUMBER: US/09/780,669
| CURRENT FILING DATE: 2001-02-09
| NUMBER OF SEQ ID NOS: 943
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO: 114
| LENGTH: 241
| TYPE: PRT
| ORGANISM: Homo sapien
US-09-759-143-114

Query Match
Best Local Similarity 100.0%; Pred. No. 1e-08; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVPAIKKDYGSOQEDFTQV 20
Db 120 LLVPAIKKDYGSOQEDFTQV 139

Search completed: February 5, 2005, 20:11:30
Job time : 75.9153 secs

Db 119 LLVPAIKKDYGSOQEDFTQV 138

RESULT 15
US-09-780-669-114
Sequence 114, Application US/09780669
GENERAL INFORMATION:
| Pat. No. US2002005197A1
| GENERAL INFORMATION:
| | APPLICANT: Xu, Jiangchun
| | APPLICANT: Dillon, Davin C.
| | APPLICANT: Mitcham, Jennifer L.
| | APPLICANT: Harlocker, Susan L.
| | APPLICANT: Jiang, Yuqui
| | APPLICANT: Henderson, Robert A.
| | APPLICANT: Kalos, Michael D.
| | APPLICANT: Fanger, Gary R.
| | APPLICANT: Retter, Marc W.
| | APPLICANT: Stolk, John A.
| | APPLICANT: Day, Craig H.
| | APPLICANT: Vedwick, Thomas S.
| | APPLICANT: Carter, Darrick
| | APPLICANT: Li, Samuel
| | APPLICANT: Wang, Ajun
| | APPLICANT: Skeiky, Yasir A.W.
| | APPLICANT: Hepler, William
| | APPLICANT: Rural, John
| | APPLICANT: McNeill, Patricia D.
| | APPLICANT: Houghton, Raymond L.
| | APPLICANT: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

| RESULT 3 | |
|-----------------|--|
| Qy | 2 LVVPAIKKDYGSQEDFTQV 20 |
| Db | : : : : : : : 329 LEPLPIKEISSVKEFTQV 347 |
| RESULT 4 | |
| Qy | 2 LVVPAIKKDYGSQEDFTQV 20 |
| Db | C;Species: Vibrio cholerae C;Accession: B82303 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; Nature, 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: B82303 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-764 <HEI> A;Cross-references: UNIPROT:Q9KUB9; GB:AE004145; PIDN:99655032; PIDN:AAF9377 A;Experimental source: serogroup O1; strain N1661; biotype El Tor C;Genetics: A;Gene: VC0603 A;Map position: 1 |
| Qy | Query Match 49.0%; Score 49; DB 2; Length 764; Best Local Similarity 45.0%; Pred. No. 7.6; Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0; |
| Db | 1 LVVPAIKKDYGSQEDFTQV 20 ::: : : : : 235 IIIAVDISTDKSQEDFTNL 254 |
| RESULT 5 | |
| Qy | 2 LVVPAIKKDYGSQEDFTQV 20 |
| Db | C;Species: Yersinia pestis C;Accession: AG0002 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hulet, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature, 413, 523-527, 2001 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AG0002 A;Status: preliminary A;Molecule type: DNA A;Cross-references: UNIPROT:Q9JJS3; GB:AL5590842; PIDN:CA88881; PID:g15978129; GSDB:G C;Genetics: A;Gene: YP00013a |
| Qy | Query Match 47.0%; Score 47; DB 2; Length 89; Best Local Similarity 60.0%; Pred. No. 1.7; Matches 9; Conservative 3; Mismatches 1; Indels 2; Gaps 1; |
| Db | 3 VVPAIKKDYGSQEDF 17 ::: : : : : 64 VVPLGLKDY- EEDF 76 |
| RESULT 5 | |
| Qy | 2 LVVPAIKKDYGSQEDFTQV 20 |
| Db | C;Species: Chlamydia muridarum (strain Nigg) C;Accession: C81726 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 R;Read, T.D.; Brunham, R.C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, |

A;Reference number: S03888 ; MUID:89211386 ; PMID:2651153
A;Accession: S03888
A;Molecule type: mRNA
A;Residues: 1-248 <WEN>
A;Cross-references: UNIPROT:P11594 ; EMBL:Y07498 ; NID:921151 ; PIDN:CAA68801.1 ; PID:982928
C;Keywords: chloroplast; photosystem II oxygen-evolving complex protein 2
C;Superfamily: chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid
F;1-62/domain: transit peptide (chloroplast) (fragment) #status predicted <TNP>
F;63-248/Product: photosystem II oxygen-evolving complex protein 2 #status predicted <MA>
Query Match 44.5%; Score 44.5; DB 2; Length 248;
Best Local Similarity 50.0%; Pred. No.13;
Matches 10; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
Qy 1 LLVVPAAKK--DYGSQEDF 17
Db 123 VMTPTDKKSITDGSPEEF 142

RESULT 11
S10016
photosystem II oxygen-evolving complex protein 2 - white mustard
N;Alternate names: photosystem II oxygen-evolving complex 23K protein
C;Species: *Sinapis alba* (white mustard)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S10016
C;Merkle, T.; Krenz, M.; Wanng, A.; Schaefer, B.
Plant Mol. Biol. 14, 889-890, 1990
A;Title: Nucleotide sequence and deduced amino acid sequence of a gene encoding the 23 k
A;Reference number: S10016 ; MUID:91346684 ; PMID:2102868
A;Accession: S10016
A;Molecule type: DNA
A;Residues: 1-260 <MER>
A;Cross-references: UNIPROT:P11594 ; EMBL:X17213 ; NID:921132 ; PIDN:CAA35081.1 ; PID:921133
C;Genetics:
A;Introns: 80/1; 158/3; 175/1
C;Superfamily: photosystem II oxygen-evolving complex protein 2
C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid
Query Match 44.5%; Score 44.5; DB 2; Length 260;
Best Local Similarity 50.0%; Pred. No.13;
Matches 10; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
Qy 1 LLVVPAAKK--DYGSQEDF 17
Db 135 VMTPTDKKSITDGSPEEF 154

RESULT 12
JC5271
oxygen-evolving complex 23K protein - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC5271
R;Kochhar, A.; Khurana, J.P.; Tyagi, A.K.
DNA Res. 3, 199, 1996
A;Title: Nucleotide sequence of the psbP gene encoding precursor of 23-kDa polypeptide of
omniphrogenic mutant.
A;Reference number: JC5271 ; MUID:97191538 ; PMID:9039496
A;Accession: JC5271
A;Molecule type: DNA
A;Residues: 1-263 <KOC>
A;Cross-references: UNIPROT:O42029 ; EMBL:X98108 ; NID:91769904 ; PIDN:CAA66785.1 ; PID:G176
C;Comment: This protein is necessary for photosystem II to be fully functional in vivo.
C;Genetics:
A;Gene: psbP
A;Introns: 83/1; 160/3; 172/3
C;Superfamily: photosystem II oxygen-evolving complex protein 2
C;Keywords: chloroplast; thylakoid
Query Match 44.5%; Score 44.5; DB 2; Length 263;
Best Local Similarity 50.0%; Pred. No.14;

Matches 10; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
Qy 1 LLVVPAAKK--DYGSOEDF 17
Db 138 VMTPTDKKSITDGSPEEF 157

RESULT 13
S00005
photosystem II oxygen-evolving complex protein 2 Precursor - spinach
N;Alternate names: water-splitting complex extrinsic membrane protein 23K chain
C;Species: Spinacia olaracea (spinach)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00005 ; S03272
R;Jansen, T.; Rothe, C.; Stegmann, J.; Reinke, H.; Beyreuther, K.; Jansson, C.; Andersson
FEBS Lett. 216, 234-240, 1987
A;Title: Nucleotide sequence of cDNA clones encoding the complete '23 kDa' and '16 kDa' I
A;Reference number: S00005
A;Accession: S00005
A;Molecule type: mRNA
A;Residues: 1-267 <CTAN>
A;Cross-references: UNIPROT:P12302
A;Note: part of this sequence, including the amino end of the mature protein, was confirm
R;Murata, N.; Kajiura, H.; Fujimura, Y.; Miyao, M.; Murata, T.; Watanabe, A.; Shinozaki,
Prog. Photosyn. Res. 1, 701-704, 1987
A;Title: Partial amino acid sequences of the proteins of pea and spinach photosystem II <
A;Reference number: S03272
A;Accession: S03272
A;Molecule type: Protein
A;Residues: 82-117 <MDR>
C;Superfamily: photosystem II oxygen-evolving complex protein 2 #status Predicted <TPN>
F;1-81/Domain: transit peptide (chloroplast) #status Predicted <TPN>
F;82-267/Product: photosystem II oxygen-evolving complex protein 2 #status experimental <
Query Match 44.5%; Score 44.5; DB 2; Length 267;
Best Local Similarity 55.0%; Pred. No.14;
Matches 11; Conservative 2; Mismatches 4; Indels 3; Gaps 1;
Qy 1 LLVVPAAKK--DYGSOEDF 17
Db 142 VLVQPTDKKSITDGSPEEF 161

RESULT 14
H8271
conserved hypothetical protein VC0037 [imported] - *Vibrio cholerae* (strain N16961 serogr
C;Species: *Vibrio cholerae*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H8271
R;Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
I., R.R.; Mekalanos, J.J.; Ventler, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035 ; MUID:20406833 ; PMID:10952301
A;Accession: H8271
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-92 <HEI>
A;Cross-references: UNIPROT:Q9KVV2 ; GB:AE004096 ; NID:99654440 ; PIDN:AAF93215
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0037
A;Map position: 1

Query Match 44.0%; Score 44; DB 2; Length 92;
Best Local Similarity 53.3%; Pred. No. 54;
Matches 8; Conservative 4; Mismatches 1; Indels 2; Gaps 1;
Qy 3 VVPAIKKDYGSOEDF 17
Db 68 VVPLGLKDDY--BDDF 80

RESULT 15
E70302 molybdenum cofactor biosynthesis protein A - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: E70302
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: E70302
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-402 <AOF>
A;Cross-references: UNIPROT:O66448; GB:AB0006570; NID:g2982779; PIDN: AAC0640
A;Experimental source: strain VF5
C;Genetics:
A;Gene: moeA
C;Superfamily: Molybdenum cofactor molybdenum incorporation protein MoeA
Query Match 44.0%; Score 44; DB 1; Length 402;
Best Local Similarity 57.9%; Pred. No. 26;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Qy 1 LLVVPALKDGSQEDTQ 19
Db 309 LLVVPALKAMQHREVFKQ 327

Search completed: February 5, 2005, 20:05:42
Job time : 20.661 secs

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| Scoring table: | BLOSUM62 | | | | | | |
|--|--|-------|-------|--------|------------|----|-------------------------------|
| Gapop: | 10.0 , Gapext: 0.5 | | | | | | |
| Searched: | 1612378 seqs, 512079187 residues | | | | | | |
| Total number of hits satisfying chosen parameters: | 1612378 | | | | | | |
| Minimum DB seq length: | 0 | | | | | | |
| Maximum DB seq length: | 2000000000 | | | | | | |
| Post-processing: | Minimum Match 0% Maximum Match 100% | | | | | | |
| Database : | UniProt 03: 1: uniprot_sprot: 2: uniprot-trembl: * | | | | | | |
| Pred. | No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | |
| SUMMARIES | | | | | | | |
| Result No. | Query | Score | Match | Length | DB | ID | Description |
| 1 | 100 | 100.0 | 241 | 1 | TSN1_HUMAN | | 060615 homo sapien |
| 2 | 84 | 84.0 | 240 | 2 | Q9J59 | | Q9J59 mus musculus |
| 3 | 76 | 76.0 | 241 | 2 | QAYR9 | | Q6ayr9 rattus norvegicus |
| 4 | 51 | 51.0 | 548 | 2 | Q8I3H5 | | Q8I3H5 plasmidium |
| 5 | 50.5 | 50.5 | 253 | 2 | Q734B0 | | Q734B5 bacillus cereus |
| 6 | 49 | 49.0 | 347 | 2 | QBYLU3 | | Q8YLu3 anaerobius sp |
| 7 | 49 | 49.0 | 764 | 2 | Q9KUB9 | | Q9Kub9 vibrio cholerae |
| 8 | 48 | 48.0 | 173 | 2 | Q9P919 | | Q9P919 pneumocystis jirovecii |
| 9 | 47 | 47.0 | 89 | 2 | Q6EGG7 | | Q66967 yersinia pestis |
| 10 | 47 | 47.0 | 89 | 2 | Q9RB12 | | Q9rb12 pectobacterium |
| 11 | 47 | 47.0 | 89 | 2 | Q8ZJSS | | Q8zjss yersinia pestis |
| 12 | 47 | 47.0 | 89 | 2 | Q6DB80 | | Q6db80 erwinia carotovora |
| 13 | 47 | 47.0 | 172 | 2 | Q9PL73 | | Q9pl73 chlamydia m |
| 14 | 46 | 46.0 | 74 | 2 | Q8LTSS | | Q8ltss lactococcus |
| 15 | 46 | 46.0 | 74 | 2 | Q779I0 | | Q779i0 lactococcus |
| 16 | 46 | 46.0 | 74 | 2 | Q9G0E7 | | Q9g0e7 lactococcus |
| 17 | 46 | 46.0 | 107 | 2 | Q6FD93 | | Q6fd93 acinetobacter |
| 18 | 46 | 46.0 | 303 | 2 | Q7WVY1 | | Q7wvy1 streptococcus |
| 19 | 46 | 46.0 | 303 | 2 | QBYAM0 | | Q8yam0 listeria monocytogene |
| 20 | 46 | 46.0 | 303 | 2 | Q724V8 | | Q724v8 listeria monocytogene |
| 21 | 45.5 | 45.5 | 600 | 2 | Q7VD65 | | Q7vd65 picrophorococcus |
| 22 | 45 | 45.0 | 88 | 2 | Q65QUS | | Q65qus manheimia |
| 23 | 45 | 45.0 | 101 | 1 | R824METMA | | Q6fd83 acinetobacter |
| 24 | 45 | 45.0 | 222 | 2 | Q6B7S8 | | Q7wvy1 streptococcus |
| 25 | 45 | 45.0 | 255 | 2 | Q93H75 | | Q8yam0 listeria monocytogene |
| 26 | 45 | 45.0 | 264 | 2 | Q7VFHS | | Q724v8 listeria monocytogene |
| 27 | 45 | 45.0 | 268 | 1 | PSP1_TOBAC | | Q7vd65 picrophorococcus |
| 28 | 45 | 45.0 | 268 | 2 | Q40457 | | Q65qus manheimia |
| 29 | 45 | 45.0 | 470 | 2 | Q7PYT9 | | Q6fd93 acinetobacter |
| 30 | 45 | 45.0 | 601 | 2 | Q7PT9 | | Q7wvy1 streptococcus |
| 31 | 45 | 45.0 | 737 | 2 | Q7KPJ2 | | Q8yam0 listeria monocytogene |

- | | | |
|------------|-------------------|---|
| - | - | SUBCELLULAR LOCATION: Integral membrane protein (Probable). |
| CC | - | SIMILARITY: Belongs to the tetraspanin (TM4SF) family. |
| CC | CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). |
| CC | CC | EMBL; AF056838; AAC69714.1; -. |
| CC | DR | DR GO; GO:0016021; C:integral to membrane; TAS. |
| CC | DR | DR InterPro; IPR00952; Tetraspanin. |
| CC | DR | DR InterPro; IPR000301; Transmem_4. |
| CC | DR | PFam; PF00335; Retrapspanin; 1. |
| CC | DR | PRINTS; PRO00259; TMFOUR. |
| CC | DR | PROSITE; PS000421; TM4.1; FALSE_NEG. |
| CC | KW | GLycoprotein, Transmembrane. |
| CC | FT | DOMAIN 1 11 Cytoplasmic (Potential). |
| CC | FT | TRANSMEM 12 32 Cytoplasmic (Potential). |
| CC | FT | DOMAIN 3 3 52 Extracellular (Potential). |
| CC | FT | TRANSMEM 5 3 73 Cytoplasmic (Potential). |
| CC | FT | DOMAIN 7 4 98 Cytoplasmic (Potential). |
| CC | FT | TRANSMEM 8 9 109 Extracellular (Potential). |
| CC | FT | DOMAIN 11 0 211 Potential. |
| CC | FT | TRANSMEM 21 2 232 Extracellular (Potential). |
| CC | FT | DOMAIN 23 3 241 Cytoplasmic (Potential). |
| CC | FT | TRANSMEM 53 3 73 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | DOMAIN 74 4 98 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | TRANSMEM 89 9 109 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | DOMAIN 110 10 211 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | TRANSMEM 212 11 232 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | DOMAIN 233 12 241 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | CARBONYD 141 1 154 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | CARBONYD 154 1 154 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | CARBONYD 178 178 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | CARBONYD 184 184 N-Linked (GlcNAc. . .) (Potential). |
| CC | FT | CARBONYD 189 189 K > E (In Ref. 1). (Potential). |
| CC | FT | CONFLICT 189 189 K > E (In Ref. 1). (Potential). |
| CC | SQ | 241 AA; 26301 MW; AF938A7D17/CB884 CRC64; |
| CC | CC | Query Match 100.0%; Score 100; DB 1; Length 241; |
| CC | CC | Best Local Similarity 100.0%; Pred. No. 1.e-08; |
| CC | CC | Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| CC | CC | Qy 1 LIIVPAIKKDKYGSQEDFTQV 20 |
| CC | CC | Db 120 LIIVPAIKKDKYGSQEDFTQV 139 |
| RESULT 2 | | |
| Q99J59 | ID | Q99J59 PRELIMINARY; PRT; 240 AA. |
| AC | AC | Q99J59; PRELIMINARY; PRT; 240 AA. |
| DT | DT | 01-JUN-2001 (TREMBLrel. 17, Created) |
| DT | DT | 01-JUN-2001 (TREMBLrel. 17, Last sequence update) |
| DT | DT | 25-OCT-2004 (TREMBLrel. 28, Last annotation update) |
| DB | DB | RIKEN cDNA 9030418M05 (Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:303 0418M05 product:similar to tetraspanin TSPAN_1). |
| DE | DE | Name=9030418M05Rik; |
| GN | GN | Mus musculus (Mouse). |
| OS | OS | Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi. |
| OC | OC | Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus. |
| NCBI_TaxID | NCBI_TaxID=10090; | [1] |
| RN | RN | SEQUENCE FROM N.A. |
| RP | RP | STRAIN=NMR1; TISSUE=Mammary tumor; MEDLINE=22308825; PubMed=12477932; DOI=10.1073/pnas.2422603899; |
| RC | RC | Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schaefer C.P., Bhat N.K., Altenschul S.P., Zeeberg B.R., Buetow K.H., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Atkins J.F., et al. |

| | | |
|----|---|---|
| RA | Kawai J., Kojima Y., Korino H., Kouda M., Koya S., Kuribara C., Ohno M., Numazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibusawa A., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagamori M., Tagami T., Yamamoto T., Yasunishi A., Tejima Y., Toya T., Yamanaka I., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashi zaki Y.; Submitted (APR-2002) to the EMBL/GenBank/DBJ databases. | DR EMBL; BC078938; AAH78938.1; -. DR GO; GO:0016021; C:Integral membrane; IEA. |
| RA | InterPro; IPR002229; RheusURHD. | DR InterPro; IPR002229; RheusURHD. |
| RA | InterPro; IPR008952; Tetraspanin. | DR InterPro; IPR008952; Tetraspanin. |
| RA | Pfam; PF00335; Tetraspanin; 1. | DR Pfam; PF00335; Tetraspanin; 1. |
| RA | PRINTS; PR00342; RHEUSURHD. | DR PRINTS; PR00342; RHEUSURHD. |
| RL | PROSITE; PS00421; TMPOUR. | DR PROSITE; PS00421; TM4.1.1. |
| DR | EMBL; BC003448; AAH03448.1; -. DR MGD; MGI:1914055; 9030418n05Rik. | SQ SEQUENCE 241 AA; 26453 MW; 9118E865464DA70 CRC64; GO; GO:0005615; C:extracellular space; TAS. |
| DR | GO; GO:0016021; C:integral membrane; TAS. | Query Match 76.0%; Score 76; DB 2; Length 241; Best Local Similarity 78.9%; Pred. No. 0.00019; Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0; |
| DR | InterPro; IPR002229; Tetraspanin. | DR InterPro; IPR002229; Tetraspanin. |
| DR | InterPro; IPR008952; Tetraspanin. | DR InterPro; IPR008952; Tetraspanin. |
| DR | PFam; PF00335; Tetraspanin; 1. | DR PFam; PF00335; Tetraspanin; 1. |
| DR | PRINTS; PR00342; RHEUSURHD. | DR PRINTS; PR00342; RHEUSURHD. |
| DR | PROSITE; PS00421; TM4.1.1. | DR PROSITE; PS00421; TMPOUR. |
| SQ | SEQUENCE 240 AA; 26356 MW; AD4C448A32BC2999 CRC64; | RESULT 4 |
| DR | EMBL; AK078869; BAC07431.1; -. DR MGD; MGI:1914055; 9030418n05Rik. | Q8I3HS PRELIMINARY; PRT; 548 AA. |
| DR | GO; GO:0005615; C:extracellular space; TAS. | AC Q8I3HS PRELIMINARY; PRT; 548 AA. |
| DR | GO; GO:0016021; C:integral membrane; TAS. | AC Q8I3HS PRELIMINARY; PRT; 548 AA. |
| DR | InterPro; IPR002229; Tetraspanin. | DT 01-MAR-2003 (TREMBLrel. 23, Created) |
| DR | InterPro; IPR008952; Tetraspanin. | DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update) |
| DR | PFam; PF00335; Tetraspanin; 1. | DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update) |
| DR | PRINTS; PR00342; RHEUSURHD. | DE Sugar transporter, putative. |
| DR | PROSITE; PS00421; TM4.1.1. | GN Name:PF01455w; |
| DR | EMBL; BC003448; AAH03448.1; -. DR MGD; MGI:1914055; 9030418n05Rik. | OS Plasmodium falciparum (isolate 3D7). |
| DR | GO; GO:0005615; C:extracellular space; TAS. | OC Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium. |
| DR | GO; GO:0016021; C:integral membrane; TAS. | NCBI_TaxID=36329; RN [1] |
| DR | InterPro; IPR002229; Tetraspanin. | RN NCBITaxonID=36329; |
| DR | InterPro; IPR008952; Tetraspanin. | RN |
| DR | PFam; PF00335; Tetraspanin; 1. | RP SEQUENCE FROM N.A. |
| DR | PRINTS; PR00342; RHEUSURHD. | RP ID Q8I3HS PRELIMINARY; PRT; 548 AA. |
| DR | PROSITE; PS00421; TM4.1.1. | AC Devlin K., Baker S., Davies P., Mungall K., Herriman M., Pain A., Hall N., Bowman S., Churcher C., Quail M., Barrell B., Hall N., Pain A., Baker S., Barron A., Brooks K., Burrows C.O., Cherevach I., Chillingworth C., Chillingworth T., Chrisdoulou Z., Clark L., Clark R., Corton C., Cronin A., Davies R., Dear P., Dearden F., Doggett J., Felthwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A., Knights A., Konfortov B., Kyes S., Lazke N., Lawson D., Leonard N., Line A., Maddison M., McLean J., Mooney P., Moulle S., Murphy L., Rajandream M.A., Rutter S., Rutherglen K.M., Sanders M., Simmonds M., Seeger S., Smith R., Squares R., Stevens K., Taylor K., Tivey A., Unwin L., Woodward J., Sulston J.E., Craig A., Newbold C., Barrell B.G., RT Nature 419:522-531(2002). |
| DR | EMBL; AL929356; CAD5163.1; -. DR MGD; MGI:1914055; 9030418n05Rik. | DR EMBL; AL929356; CAD5163.1; -. DR MGD; MGI:1914055; 9030418n05Rik. |
| DR | GO; GO:0005615; C:extracellular space; TAS. | SQ SEQUENCE 548 AA; 63788 MW; 245CACD595067CF3 CRC64; |
| DR | GO; GO:0016021; C:integral membrane; TAS. | Query Match 51.0%; Score 51; DB 2; Length 548; Best Local Similarity 50.0%; Pred. No. 9.1; Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0; |
| DR | InterPro; IPR002229; Tetraspanin. | Q8I3HS PRELIMINARY; PRT; 548 AA. |
| DR | InterPro; IPR008952; Tetraspanin. | Q8I3HS PRELIMINARY; PRT; 548 AA. |
| DR | PFam; PF00335; Tetraspanin; 1. | Q8I3HS PRELIMINARY; PRT; 548 AA. |
| DR | PRINTS; PR00342; RHEUSURHD. | Q8I3HS PRELIMINARY; PRT; 548 AA. |
| DR | PROSITE; PS00421; TM4.1.1. | Q8I3HS PRELIMINARY; PRT; 548 AA. |
| DR | EMBL; BC003448; AAH03448.1; -. DR MGD; MGI:1914055; 9030418n05Rik. | RESULT 5 |
| DR | GO; GO:0005615; C:extracellular space; TAS. | Q734B5 PRELIMINARY; PRT; 253 AA. |
| DR | GO; GO:0016021; C:integral membrane; TAS. | Q734B5 PRELIMINARY; PRT; 253 AA. |
| DR | InterPro; IPR002229; Tetraspanin. | Q734B5 PRELIMINARY; PRT; 253 AA. |
| DR | InterPro; IPR008952; Tetraspanin. | Q734B5 PRELIMINARY; PRT; 253 AA. |
| DR | PFam; PF00335; Tetraspanin; 1. | Q734B5 PRELIMINARY; PRT; 253 AA. |
| DR | PRINTS; PR00342; RHEUSURHD. | Q734B5 PRELIMINARY; PRT; 253 AA. |
| DR | PROSITE; PS00421; TM4.1.1. | Q734B5 PRELIMINARY; PRT; 253 AA. |
| DR | EMBL; BC003448; AAH03448.1; -. DR MGD; MGI:1914055; 9030418n05Rik. | RN SEQUENCE FROM N.A. |
| DR | GO; GO:0005615; C:extracellular space; TAS. | RC TISSUE=Kidney. |
| DR | GO; GO:0016021; C:integral membrane; TAS. | RC TISSUE=Kidney. |
| DR | InterPro; IPR002229; Tetraspanin. | RC Director MGC Project. |
| DR | InterPro; IPR008952; Tetraspanin. | RC Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases. |

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE CAAx amino terminal protease family.
 GN OrderedLocusNames=BCE3192;
 Bacillus cereus (strain ATCC 10987).
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=222523;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=14960714; DOI=10.1093/nar/gkh258;
 RA Rasko D.A., Ravel J., Oekstaad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.E., Tournasse N.J., Angiuoli S.V., Kolonay J.P.,
 RA Nelson W.C., Kolsjoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
 adaptations and a large plasmid related to *Bacillus anthracis* pXO1.";
 RL EMBL; AF017275; ARS42398.1; -.
 DR TIGR; BC3492; -.
 DR GO; GO:000233; F:peptidase activity; IEA.
 DR InterPro; IPR003675; Abi.
 DR Pfam; PF0251; Abb; 1.
 KW Complete proteome; Protease;
 SEQUENCE 253 AA; 28985 MW; 9572AA6F36352785 CRC64;

Query Match 50.5%; Score 50.5; DB 2; Length 253;
 Best Local Similarity 55.0%; Pred. No. 4; 7;
 Matches 11; Conservative 3; Mismatches 1; Indels 5; Gaps 1;

QY 3 VVPAl----KKDYGSQEDE 17
 Db 48 IMPAIAlSLKkYGSQEDE 67

RESULT 6

O8YLU3 Q8YLU3 PRELIMINARY; PRT; 347 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Alr5203 protein.
 GN OrderedLocusNames=alr5203;
 OC Anaerobium sp. (strain PCC 7120).
 NCBI_TaxID=103690;

RN [1]
 RP SEQUENCE FROM N.A. MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takayama M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium *Anabaena* sp. strain PCC 7120.",
 DNA Res 8:205-213(2001);
 DR EMBL; AP003539; BAB76902.1; -.
 DR PIR; AC2456; AC2456.
 DR PRO535; Glycos_transf_2; 1.
 KW Complete proteome;
 SEQUENCE 347 AA; 40541 MW; APBC249221FBB26D CRC64;

Query Match 49.0%; Score 49; DB 2; Length 347;
 Best Local Similarity 55.6%; Pred. No. 12; Mismatches 5; Indels 0; Gaps 0;

QY 2 LVVPAIKKDKYGSQEDFTQV 20
 Db 329 LEPLTIKKRISVKEFTQV 347

RESULT 7

Q9KUB9 Q9KUB9 PRELIMINARY; PRT; 764 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE Hypothetical protein VC0603.
 GN OrderedLocusNames=VC0603;
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrioaceae; Vibrio.

RN [1]
 RP SEQUENCE FROM N.A. STRAIN=SEL Tor NT16961 / Serotype O1:
 RX MEDLINE=20406831; PubMed=10952301; DOI=10.1088/350200000;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.B., Read T.D., Tettelin H., Richardson D.L.,
 RA Brzuska M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
 RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
 RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
 RA Mekalanos J.J., Venter J.C., Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio
 cholerae*.", Nature 406:477-483 (2000);
 RL EMBL; AE0004145; AAFC92770.1; -.
 DR PIR; BB2303; BB2303.
 DR TIGR; VC0603; -.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR CO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0045735; F:nucleic acid reservoir activity; IEA.
 DR InterPro; IPR00994; Nucleic_acid_QB.
 DR InterPro; IPR002641; Patatin.
 DR Pfam; PF01734; Patatin; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 764 AA; 85616 MW; 0C3C8BCA100CC040 CRC64;

RESULT 8

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 LLVVPAlKKDKYGSQEDFTQV 20
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 9

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 10

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 11

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 12

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 13

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 14

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 15

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 16

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 17

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 18

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 19

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 20

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 21

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 22

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 23

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 24

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 25

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 26

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 27

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 28

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 29

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 30

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 31

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 32

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 33

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 34

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 35

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 36

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 37

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 38

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 39

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 40

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 41

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 42

Q9PP919 Q9PP919 PRELIMINARY; PRT; 173 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

QY 1 Pneumocystis carinii f. sp. suis.
 Db 235 IIIAVD1STDYKQSQEDFTNL 254

Query Match 49.0%; Score 49; DB 2; Length 764;
 Best Local Similarity 45.0%; Pred. No. 29; Mismatches 7; Indels 0; Gaps 0;

DB 235 IIIAVD1STDYKQSQEDFTNL 254

RESULT 43

| | | | | |
|-----------------------|---|--------------------------------|--|---|
| CC | family | EMBL; AF146755; AAF25727.1; -. | DT | 01-MAR-2004 (TREMBLrel. 26, Last annotation update) |
| DR | HSSP; Q9240; 1KC.C. | DE | YihD. | |
| DR | GO; GO:0046872; F:metal ion binding; IEA. | GN | Name=yihD. | |
| DR | GO; GO:0016491; F:oxidoreductase activity; IEA. | OS | Pectobacterium carotovorum (subsp. carotovorum) (Erwinia carotovora (subsp. carotovora)). | |
| DR | GO; GO:0004784; F:superoxide dismutase activity; IEA. | OS | Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; | |
| DR | GO; GO:0006801; P:superoxide metabolism; IEA. | OC | Enterobacteriaceae; Pectobacterium. | |
| DR | InterPro; IPR001189; SODIsmutase. | OC | NCBI_TaxID=555; | |
| DR | Pfam; PF02777; Sod_Fe_C; 1. | OX | [1]_TaxID=555; | |
| DR | Pfam; PF00081; Sod_Fe_N; 1. | RN | RN | |
| DR | PRINTS; PRO1703; MNSODISMTASE. | RP | SEQUENCE FROM N.A. | |
| DR | Prodrom; PDD00475; SODismtase; 1. | STRAIN | SCR1193; | |
| DR | PROSITE; PS000088; SOD_MN; 1. | RX | MEDLINE=93392457; PubMed=10463161; | |
| KW | Oxidoreductase. | RA | Vincent-Sealy L.V., Thomas J.D., Commander P., Salmon G.P., | |
| PT | NON_TER 1 1 | RT | "Erwinia carotovora Dsba mutants: evidence for a periplasmic-stress signal transduction system affecting transcription of genes encoding secreted proteins." | |
| FT | NON_TER 173 173 | RT | RT | |
| SQ | SEQUENCE 173 AA; 20099 MW; 69110EPFD0005665B CRC64; | RT | Microbiology 145:1945-1958 (1999). | |
| Query Match | 48.0%; Score 48; DB 2; Length 173; | RL | MEDLINE=146615; Aad47615.1; -. | |
| Best Local Similarity | 50.0%; Pred. No. 8.3; | DR | InterPro; IPR009383; DUF1040. | |
| Matches | 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0; | DR | Pfam; PF06288; DUF1040; 1. | |
| Qy | 3 VVPAIKKDYGSQEDFQV 20 | SQ | SEQUENCE 89 AA; 10402 MW; 228FDD71E865481 CRC64; | |
| Db | 85 LVEAIKKEWGSGVNFPSI 102 | Query | 3 VVPAIKKDYGSQEDF 17 | |
| RESULT 9 | Q66GG7 PRELIMINARY; PRT; 89 AA. | Query Match | 47.0%; Score 47; DB 2; Length 89; | |
| ID | Q66GG7 | Best Local Similarity | 60.0%; Pred. No. 5.8; | |
| AC | Q66GG7; | Matches | 3; Mismatches 3; Gaps 1; | |
| DT | 25-OCT-2004 (TREMBLrel. 28, Created) | Db | 64 VIPGLKKDY--EEDF 76 | |
| DT | 25-OCT-2004 (TREMBLrel. 28, Last sequence update) | RESULT 11 | | |
| DE | Hypothetical protein. | ID | Q8ZQS3 PRELIMINARY; PRT; 89 AA. | |
| GN | ORFName=xPTB0015; | AC | Q8ZQS3; Q74YDD; Q7CG24; | |
| OS | Yersinia pseudotuberculosis IP 32953. | DT | 01-MAR-2002 (TREMBLrel. 20, Created) | |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; | DT | 01-MAR-2002 (TREMBLrel. 20, Last sequence update) | |
| OC | Enterobacteriaceae; Yersinia. | DT | 25-OCT-2004 (TREMBLrel. 28, Last annotation update) | |
| NCBI_TaxID | 273123; | DB | Hypothetical protein YP00013a (Hypothetical protein y3814). | |
| RN | [1] | GN | Name=YP00013a; OrderediticusNames=YP0015, y3814; | |
| OS | Yersinia pestis B. | OS | Yersinia pestis B. | |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales. | OC | Bacteria; Proteobacteria; Enterobacteriaceae; Yersinia. | |
| RX | SEQUENC FROM N.A. | OC | NCBI_TaxID=632; | |
| RX | STRAIN=IP 32953; | OX | [1]_TaxID=632; | |
| RA | Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O., | RN | RN | |
| RA | Regala W.M., Georgescu A.M., Vergez L.W., Land M.L., Motin L.V., | RP | SEQUENCE FROM N.A. | |
| RA | Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C., | RC | STRAIN=CO-92 / Biovar Orientalis; | |
| RA | Simonet M., Chenal-francisque V., Souza B., Dacheux D., Elliott J.M., | RX | MEDLINE=21470413; PubMed=11566360; DOI=10.1038/350907083; | |
| RA | Derbise A., Hauser L.J., Garcia E.; | RA | Parthill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., | |
| RT | "Insights into the genome evolution of Yersinia pestis through whole | RA | Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L., | |
| RT | genomic comparison with Yersinia pseudotuberculosis."; | RA | Baker S., Basam D., Bentley S.D., Brooks K., Cedeno-Tarrega A.-M., | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004). | RA | Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., | |
| DR | EMBL; BX316398; CAH19255.1; -. | RA | Felwell T., Hamlin N., Holloway S., Jagels K., Karlyshev A.V., | |
| DR | InterPro; IPR009383; DUF1040. | RA | Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherdale K.M., | |
| DR | Pfam; PF06288; DUF1040; 1. | RA | Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., | |
| KW | Hypothetical protein. | RA | "Genome sequence of Yersinia pestis, the causative agent of plague."; | |
| SQ | SEQUENC 89 AA; 10168 MW; C240C03A620D66F9 CRC64; | RT | Nature 413:525-527(2001). | |
| Query Match | 47.0%; Score 47; DB 2; Length 89; | RL | [2] | |
| Best Local Similarity | 60.0%; Pred. No. 5.8; | RP | SEQUENCE FROM N.A. | |
| Matches | 9; Conservative 3; Mismatches 1; Indels 2; Gaps 1; | RC | STRAIN=KIMS / Biovar Mediaevalis; | |
| Qy | 3 VVPAIKKDYGSQEDF 17 | RX | MEDLINE=22137863; PubMed=12142430; | |
| Db | 64 VIPGLKKDY--EEDF 76 | RA | DOI=10.1128/JB.184.16.4601-4611.2002; | |
| RESULT 10 | Q9RB12 PRELIMINARY; PRT; 89 AA. | RA | Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.P., Liiss P., | |
| ID | Q9RB12; | RA | Perra N.T., Rose D.J., Mau B., Schwartz D.C., Zhou S., | |
| AC | AC | RA | Fetherston J.D., Lindler L.E., Brubaker R.R., Piano G.V., | |
| DT | 01-MAY-2000 (TREMBLrel. 13, Created) | RA | Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., | |
| DT | 01-MAY-2000 (TREMBLrel. 13, Last sequence update) | RA | Perry R.D.; | |
| | | RT | "Genome sequence of Yersinia pestis KIM."; | |
| | | RL | J. Bacteriol. 184:4601-4611(2002). | |
| | | RN | [3] | |
| | | RP | SEQUENCE FROM N.A. | |
| | | RC | STRAIN=91001 / Biovar Mediaevalis; | |
| | | RA | Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D., | |

Page 6

| | | |
|---|---|---|
| RA | Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R., Submitted (APR-2003) to the EMBL/GenBank/DBJ databases. | OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia. NCBI_TaxID=83560; |
| RL | EMBL; AJ414141; CAC88811; -; | SEQUENCE FROM N.A. |
| DR | DR/ AE013984; AMB/359..1; -; | STRAIN=MOPN / Niqq9; |
| DR | DR/ AE017127; AAS60296..1; -; | RC MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/gkz1397; |
| PIR | PIR; AG002; AG002; | Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickie B.K., Peterson J.D., Utterback T.R., Berry K.J., Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C., Dodson R.J., Gwinn M.L., Nelson W.C., Deboy R.T., Kolonay J.F., McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.; RT "Genome sequence of Chlamydia trachomatis MoPn and Chlamydia pneumoniae Ar39."; RT Nucleic Acids Res. 28:1397-1406 (2000). |
| KW | Complete proteome; Hypothetical protein. | DR EMBL; AB02230; AAF39106.1; -. |
| SQ | SEQUENCE 89 AA; 10168 MW; C240C03A620D66F9 CRC64; | DR PIR; CB1726; C81726. |
| Query Match | Score 47; DB 2; Length 89; | TIGR; TC0235; DR InterPro; IPR007966; DUF720. |
| Best Local Similarity | 60.0%; Pred. No. 5.8; | DR Pfam; PF05302; DUF720; 1. |
| Matches | 3; Mismatches 1; Indels 2; Gaps 1; | KW Complete proteome; Hypothetical protein. |
| Qy | 3 VVPAIKKDYGQSQEDF 17 | SQ SEQBNCE 172 AA; BB6AAC64AA88AAAB CRC64; |
| Db | 64 VTFGLKDKY--BEDF 76 | Query Match Score 47; DB 2; Length 172; Best Local Similarity 44.4%; Pred. No. 12; Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0; |
| RESULT 12 | Q6DBB0 PRELIMINARY; PRT; 89 AA. | RESULT 14 Q8LT55 PRELIMINARY; PRT; 74 AA. |
| AC | Q6DBB0 PRELIMINARY; | ID Q8LT55; PRELIMINARY; |
| DT | DT 25-OCT-2004 (TREMBLrel. 28, Created) | ID DT 01-OCT-2002 (TREMBLrel. 22, Created) |
| DT | DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update) | DT DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update) |
| DT | DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update) | DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) |
| DE | Hypothetical protein. | DB Putative cro-like repressor. |
| GN | OrderedLocusName=ECA0018; | OS Lactococcus lactis bacteriophage ul36. |
| GS | Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum). | OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae. |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; | OX NCBI_TaxID=29471; |
| OC | Enterobacteriaceae; Pectobacterium. | RN SEQUENCE FROM N.A. |
| CX | NCP_29471; | RP MEDLINE=2206604; PubMed=12069529; DOI=10.1006/viro.2002.1401; |
| RN | SEQUENCE FROM N.A. | RX Labrie S., Moineau S; |
| RC | STRAIN=SCR1 1043 / ATCC BA-672; | RT "Complete genomic sequence of bacteriophage ul36: demonstration of phage heterogeneity within the P35 quasi-species of lactococcal phages.", RT Virology 296:308-320 (2002). |
| RR | PUBMED=15263089; DOI=10.1073/phas.0402424101; | RR DR AF329457; AAM75754.1; -. |
| RA | Bell K.S., Sebastian M., Pritchard L., Holden M.T.G., Hyman L.J., Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K., Atkin R., Basin N., Brooks K., Chillingworth T., Clark K., Doggett J., Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norberczak H., Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S., Salmon G.P.C., Birch P.R.J., Parkhill J., Toth I.K.; | DR IntezPro; IPR008003; DUF739. |
| RT | "Genome sequence of the enterobacterial phytopathogen <i>Erwinia carotovora</i> subsp. atroseptica and characterization of virulence factors."; RT DR IntezPro; IPR010982; Lambda_like_DNA. | |
| RR | Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004). | DR PF05339; DUF739.1; -. |
| RL | DR IMER; BX950851; CGG72942.1; -. | DR Sequence 74 AA; 8559 MW; B42AF1806FAB767 CRC64; |
| DR | DR InterPro; IPR009363; DUF1040. | Query Match Score 46; DB 2; Length 74; Best Local Similarity 61.5%; Pred. No. 7.1; Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0; |
| PIR | PIR; PF06288; DUF1040; 1. | Qy 7 IKKDYGQSQEDFTQ 19 |
| KW | Complete proteome; Hypothetical protein. | Db 12 IKEKYGQQDFAK 24 |
| SQ | SEQUENCE 89 AA; 10418 MW; OCTEFDDD71E8647A0 CRC64; | Query Match Score 47; DB 2; Length 89; Best Local Similarity 60.0%; Pred. No. 5.8; Matches 3; Mismatches 1; Indels 2; Gaps 1; |
| Query | 3 VVPAIKKDYGQSQEDF 17 | RESULT 13 Q9PL73 PRELIMINARY; PRT; 172 AA. |
| Db | 64 VTFGLKDKY--BEDF 76 | ID Q9PL73; PRELIMINARY; |
| RESULT 14 Q77910 PRELIMINARY; PRT; 74 AA. | AC Q77910 PRELIMINARY; | |
| DT | DT 01-OCT-2000 (TREMBLrel. 15, Created) | AC Q77910 PRELIMINARY; |
| DT | DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) | DT DT 05-JUL-2004 (TREMBLrel. 27, Created) |
| DT | DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) | DT DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update) |
| DE | Hypothetical protein TC0235. | DE DE Putative cro repressor. |
| OrderedLocusName=B | OrderedLocusName=C | |
| Chlamydia muridarum | Chlamydia muridarum | |

```

GN Name=cro;
OS Lactococcus bacteriophage phi31.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TAXID=46654;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21141825; PubMed=11229902;
RX DOI=10.1128/AEM.67.3.1128-1139.2001;
RA Madsen S.M., Mills D., Djordjevic G., Israelsen H., Klaenhammer T.R.:
RT "Analysis of the genetic switch and replication region of a P335-type
RT bacteriophage with an obligate lytic lifestyle on Lactococcus
RT lactis.";
RL Appl. Environ. Microbiol. 67:1128-1139(2001).
DR EMBL; AJ29531; CAC04155.1; -
DR InterPro; IPR008003; DUF39.
DR InterPro; IPR010982; Lambda-like DNA.
DR PFam; PF05339; DUF739; 1.
SQ SEQUENCE 74 AA; 8533 MW; B42A2F18180B5867 CRC64;
Query Match 46.0%; Score 46; DB 2; Length 74;
Best Local Similarity 61.5%; Pred. No. 7.1;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 7 IKKDYGSQEDFTQ 19
Db 1: ||||:|||:
      12 IKBKYGQQDFAK 24

```

Search completed: February 5, 2005, 20:04:40
Job time : 97.9153 secs

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 OM protein - protein search, using sw model
 Run on: February 5, 2005, 19:34:18 ; Search time 99.5085 Seconds
 (without alignments)
 73.847 Million cell updates/sec
 Title: US-09-780-669-114_COPY_151_169
 Perfect score: 106
 Sequence: 1 GFTNTDFFSPYFKENSA 19
 Scoring table: BLOSUM62
 Gapext 0.5
 Gapop 10.0 ,
 Score: 21.05692 seqs, 386760381 residues
 Searched: Adj 46070 Novel hum
 Adj 45975 Novel hum
 Adj 45976 Novel hum
 AAG99003 Human pro
 Abu71654 Prostate
 Abn0679 Human Ar4
 Hau04962 Human pro
 Abg96414 Human ova
 Abb95223 Human NI-
 Abg76666 Prostate
 Abr54315 Prostate
 Abd75601 Prostate
 Abd13564 Human pro
 Adg25980 Human pro
 Adn39286 Cancer/an
 Abg96431 Human ova
 Abd75599 Prostate
 AAw61618 Clone HPW
 Abw01500 Human rec
 Aay36171 Human sec
 241 4 AAG99003 Human pro
 241 4 ABU71654 Prostate
 241 4 ABH90679 Human Ar4
 241 4 AAU04962 Human pro
 241 5 ABG96414 Human ova
 241 5 ABb95223 Human NI-
 241 5 ABG76666 Prostate
 241 6 ABR54315 Prostate
 241 7 ADB75601 Prostate
 241 7 ADB13564 Human pro
 241 7 ADG25980 Human pro
 241 7 ADN39286 Cancer/an
 258 5 ABG96431 Human ova
 258 7 ADB75599 Prostate
 273 2 AAw61618 Clone HPW
 273 7 ABW01500 Human rec
 43 2 AAY36171 Human sec
 43 2 AAY36218 Human sec
 43 7 ADJ45975 Novel hum
 43 7 ADJ45976 Novel hum
 43 7 ADJ46070 Novel hum

ALIGNMENTS

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

RESULT 1
AAM01157
ID AAM01157 standard; peptide; 19 AA.

Database : A_Genome_16Dec04.*
 1: genomepl980s:
 2: genomepl980s:
 AC ARM1157;
 XX

3: geneseqp2000S;*
 4: geneseqp2001S;*
 5: geneseqp2002S;*
 6: geneseqp2003AB;*
 7: geneseqp2003B;*
 8: geneseqm2004A;*
 XX Human prostate-specific peptide used in epitope mapping studies #14.
 DE XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
 KW cytosstatic; gene therapy; metastasis.
 KW YY

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

Pred. No. OS XX PN
 Homo sapiens. WO2001151633-A2.
 XX PN XX

SUMMARIES

| Result No. | Query | | | | ID | Description |
|------------|-------|-------|--------|----|----------|---------------------|
| | Score | Match | Length | DB | | |
| 1 | 106 | 100.0 | 19 | 4 | AAM01157 | Aam01157 Human pro |
| 2 | 106 | 100.0 | 19 | 4 | AAU69802 | Aau69802 Human pro |
| 3 | 106 | 100.0 | 19 | 4 | AAU99042 | Aagj9042 Human pro |
| 4 | 106 | 100.0 | 19 | 4 | ABU7193 | ABU7193 Prostate |
| 5 | 106 | 100.0 | 19 | 5 | ABB9562 | Abb9562 Epitope m |
| 6 | 106 | 100.0 | 19 | 6 | ABR54374 | ABR54374 Prostate |
| 7 | 106 | 100.0 | 19 | 7 | ADB13954 | Adb13954 Human pro |
| 8 | 106 | 100.0 | 19 | 7 | ADG26370 | Adg26370 Human pro |
| 9 | 106 | 100.0 | 172 | 7 | ADD69510 | Add69510 Human REM |
| 10 | 106 | 100.0 | 174 | 8 | ADP81123 | Adp81123 Protein o |
| 11 | 106 | 100.0 | 214 | 8 | ADR65994 | Adrs65994 Human pro |
| 12 | 106 | 100.0 | 214 | 8 | ADR66892 | Adr66892 Human pro |
| 13 | 106 | 100.0 | 233 | 2 | AAW7060 | Aaw7060 Human sec |

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate cancer.

volume. AAH9357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.

Sequence 19 AA;

| | | | | | | | |
|-----------------------|--------|------------|----------|--------|----|--------|-----|
| Query Match | 100.0% | Score | 106; | DB | 4; | Length | 19; |
| Best Local Similarity | 100.0% | Pred. No. | 6.2e-09; | | | | |
| Matches | 19; | Mismatches | 0; | Indels | 0; | Gaps | 0; |

Qy 1 GFTNYTDFEDSPYFKNSA 19
Db 1 GFTNYTDFEDSPYFKNSA 19

RESULT 2

AAU59802

AAU59802 standard; peptide; 19 AA.

XX DT 30-JAN-2002 (first entry)

XX DE Human prostate protein epitope mapping peptide #1.

XX Human; prostate cancer; ss; cytostatii; immunostimulant; tumour; antigen; epitope.

XX KW Homo sapiens.

XX PN WO200173032-A2.

XX PD 04-OCT-2001.

XX PP 27-MAR-2001; 2001WO-US009919.

XX PR 27-MAR-2000; 2000US-005336857.

PR 09-MAY-2000; 2000US-00568100.

PR 12-MAY-2000; 2000US-00570727.

PR 13-JUN-2000; 2000US-00597793.

PR 27-JUN-2000; 2000US-0060783.

PR 09-AUG-2000; 2000US-00636215.

PR 29-AUG-2000; 2000US-00651236.

PR 06-SEP-2000; 2000US-00657279.

PR 02-OCT-2000; 2000US-00679426.

PR 10-OCT-2000; 2000US-00685166.

PR 09-NOV-2000; 2000US-00705729.

PA (CORTI-) CORIXA CORP.

XX PI J. Dillon DC, Mitcham JL, Harlockier SL, Jiang Y, Kalos MD;

PI Fanger GR, Rettler MW, Stolk JA, Day CH, Vedick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Repler WT, Henderson RA;

XX WPI: 2001-639232/73.

XX The invention relates to isolated prostate-specific polypeptides useful for

PT the diagnosis and treatment of cancer, especially prostate cancer.

XX PS Claim 2: Page 400: 579pp; English.

XX The invention relates to isolated prostate-specific polynucleotides

CC polypeptides, fusion proteins of the polypeptides, antibodies raised

CC against the polypeptides (or antigenic epitopes derived from them) and

CC antigen-presenting cells expressing the polypeptides. The antibodies are

CC useful for detecting the presence of cancer, especially prostate cancer.

CC The polypeptides, polynucleotides and the antigen-presenting cells are

CC useful for stimulating and/or expanding T cells specific for a tumour

CC protein, and for inhibiting the development of cancer especially prostate

CC cancer. Compositions comprising the polynucleotide and/or polypeptide are

CC useful for stimulating an immune response, and for treating cancer. The

CC oligonucleotide is useful for detecting cancer. The present sequence is a

CC prostate specific peptide of the invention. The peptides either represent

| | |
|----|--|
| CC | antigenic epitopes or domains of prostate specific proteins |
| XX | Sequence 19 AA; |
| SQ | Query Match 100.0%; Score 106; DB 4; Length 19; Best Local Similarity 100.0%; Pred. No. 6.2e-09; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 GFTNYTDFEDSPYFKNSA 19 |
| Db | 1 GFTNYTDFEDSPYFKNSA 19 |

RESULT 3

| | |
|----------|---|
| AAG93042 | AAG93042 standard; peptide; 19 AA. |
| ID | AAG93042 |
| XX | XX Human prostate specific epitope mapping peptide #14. |
| AC | AAG93042; |
| XX | XX Human prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate specific protein; chromosome 1; prostate specific antigen; PSA. |
| XX | XX Homo sapiens. |
| OS | OS PN WO200134802-A2. |
| XX | XX PD 17-MAY-2001. |
| XX | XX PP 09-NOV-2000; 2000WO-US039904. |
| XX | XX PR 12-NOV-1999; 99US-00439313. |
| XX | PR 18-NOV-1999; 99US-00441686. |
| PA | PA (CORTI-) CORIXA CORP. |
| XX | XX Xu J, Dillon DC, Mitcham JL, Harlockier SL, Jiang Y, Reed SG; |
| PI | PI Kalos MD, Rettler MW, Stolk JA, Day CH, Skeiky YAW, Wang A; |
| XX | XX WPI; 2001-308785/32. |
| XX | XX Isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, useful in the diagnosis and therapy of prostate cancer. |
| XX | XX PT Isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, useful in the diagnosis and therapy of prostate cancer. |
| PS | PS Claim 3; Page 299; 325pp; English. |
| XX | XX The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P774P, P775P and B303D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification of the present invention |
| SQ | Sequence 19 AA; |
| CC | Query Match 100.0%; Score 106; DB 4; Length 19; Best Local Similarity 100.0%; Pred. No. 6.2e-09; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 GFTNYTDFEDSPYFKNSA 19 |
| Db | 1 GFTNYTDFEDSPYFKNSA 19 |

RESULT 4

ABU71693 ID ABU71693 standard; peptide; 19 AA.

XX AC ABU71693;

XX DT 10-JUN-2003 (first entry)

DE Prostate cancer therapy associated peptide #15.

XX KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostate specific membrane antigen; prostatic acid phosphatase; PAP; prostate specific membrane antigen; PSA.

XX KW

OS Homo Sapiens.

PN US2002192763-A1.

XX PD 19-DEC-2002.

XX PP 29-JUN-2001; 2001US-00895793.

XX PR 04-OCT-1999; 99US-0157455P.

PR 04-OCT-2000; 2000US-00679272.

PR 28-MAR-2001; 2001US-00822827.

XX PA (XUJJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAIC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A.

PA (HURA/) HURAL J. D.

PA (MCNE/) MCNEILL P D.

PA (HOUG/) HOUGHTON R L.

PA (DBAS/) Y DE BASSOLS C V.

PA (FOYT/) FOYT T M.

XX PI Xu J., Dillon DC, Mitcham JL, Harlocker SL, Jiang Y., Kalos MD, Carter D.; Panger GR, Retter MW, Stolk JA, Day CH, Vedick TS, Carter D.; Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J.; Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;

XX DR WPI: 2001-245062/2.

XX PT Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.

XX Example 18; SEQ ID NO 504; 85pp; English.

CC The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPRO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This is the amino acid sequence of a

CC prostate cancer therapy associated peptide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US Patent Office at seqdata.uspto.gov/sequence.html?DocID=US2002192763

CC XX SQ Sequence 19 AA;

Query Match 100.0%; Score 106; DB 4; Length 19;

Best Local Similarity 100.0%; Pred. No. 6; 20-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNTDFEDSPYFFKNSA 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GFTNTDFEDSPYFFKNSA 19

RESULT 5

ABB9262 ID ABB9262 standard; peptide; 19 AA.

XX AC ABB9262;

XX DT 19-JUL-2002 (first entry)

XX DE Epitope mapping study peptide SEQ ID NO 504.

XX KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; gene therapy.

XX OS Unidentified.

XX PN US2002022248-A1.

XX PD 21-FEB-2002.

XX PP 12-JAN-2001; 2001US-00759143.

XX PR 25-FEB-1997; 97US-00806099.

PR 01-AUG-1997; 97US-0094804.

PR 10-FEB-1998; 98US-00020956.

PR 25-FEB-1998; 98US-00030607.

PR 14-JUL-1998; 98US-00115453.

PR 23-SEP-1998; 98US-00159812.

PR 15-JAN-1999; 99US-00232149.

PR 09-APR-1999; 99US-00288946.

PR 13-JUL-1999; 99US-0032616.

PR 12-NOV-1999; 99US-00439313.

PR 18-NOV-1999; 99US-00443686.

PR 14-JAN-2000; 2000US-00483672.

PR 27-MAR-2000; 2000US-00536857.

PR 09-MAY-2000; 2000US-00568100.

PR 12-MAY-2000; 2000US-00570737.

PR 13-JUN-2000; 2000US-00593793.

PR 27-JUN-2000; 2000US-00605783.

PR 10-AUG-2000; 2000US-0056215.

PR 29-AUG-2000; 2000US-0051236.

PR 06-SEP-2000; 2000US-0051236.

PR 02-OCT-2000; 2000US-00579426.

PR 10-OCT-2000; 2000US-00685166.

XX PA (XUJJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.
 PA (SKEIY/) SKEIY Y A W.
 PA (HEPL/) HEPPL W T.
 PA (HEND/) HENDERSON R A.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
 PI Li SX, Wang A, Skei YAM, Hepler WT, Henderson RA;
 PI DR; 2002-255649/30.
 XX
 New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer.
 XX
 Claim 2; SEQ ID NO 504; 87pp; English.
 XX
 The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a
 CC peptide described in the invention
 XX Sequence 19 AA;
 Query Match 100.0%; Score 106; DB 5; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT
 Qy 1 GFTNYTDFDSFYFKNSA 19
 Db 1 GFTNYTDFDSFYFKNSA 19
 XX
 RESULT 7
 ADB11954
 ID ADB11954 standard; peptide; 19 AA.
 XX
 AC ADB11954;
 XX DT 18-DEC-2003 (first entry)
 DB Human prostate protein P503S epitope mapping peptide #2101.
 XX
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
 KW cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell; epitope.
 OS Homo sapiens.
 XX
 PN US2003185830-A1.
 XX PD 02-OCT-2003.
 XX
 ID ABR54374 standard; protein; 19 AA.
 XX
 AC ABR54374;
 XX DT 28-AUG-2003 (first entry)
 XX
 Prostate tumour specific related peptide for epitope mapping SEQ ID 504.
 XX
 Cytostatic; gene therapy; prostate-specific protein; PSP; human;
 KW immune response; prostate cancer.
 XX
 Homo sapiens.
 XX
 PN WO200289747-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 09-MAY-2002; 2002WO-US014753.
 XX
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-0085814.
 PR 10-DEC-2001; 2001US-00012896.
 XX
 (CORY-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carrier D, Li SX, Wang A, Skei YAM, Hepler WT, Hural J;
 PI Mcneill PD, Houghton RL, Vinalis Y De BassolsC, Foy TM, Watanabe Y;
 PI Deng T;
 XX
 DR WPI; 2003-167130/16.
 XX
 New prostate-specific proteins and genes, useful in gene therapy,
 PT particularly for stimulating an immune response in a patient, or treating
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 PT in a patient.
 XX
 PS Example 18; Page 466; 691pp; English.
 XX
 CC The present invention relates to novel prostate-specific proteins (PSP)
 CC and their coding sequences. The PSPs and their coding sequences are
 CC useful for stimulating an immune response in a patient, or for treating
 CC prostate cancer in patient and for determining, detecting or diagnosing
 CC the presence of a cancer in a patient. The present sequence was used to
 CC illustrate the invention
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 106; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PA (CORI-X) CORIXA CORP.
 XX
 PI Xu J, Stolk JA, Kalos MD;
 XX DR WPI: 2003-756133/71.
 XX PT New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate cancer.
 PT
 PT Example 18; Page: 101pp; English.
 XX CC The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB13563 comprising a sequence ADB1487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific cDNA, one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the peptides or a polypeptide appearing as ADB13558, detecting the amount of polypeptide that binds to the agent and comparing the amount of polypeptide to a predetermined cut-off value to determine the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the peptides or the isolated T cell population, treating prostate cancer in a patient comprising administering a composition comprising the peptides, nucleic acids, antibodies or compounds determining the presence of a cancer in a patient and treating prostate cancer in a patient comprising incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated from a patient with the peptides or antigen presenting cells that express (the peptides so that the T cells proliferate, and administering the proliferated T cells to the patient. The peptides (or an oligonucleotide that hybridises to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides, nucleic acids encoding, or antigen-presenting cells expressing the nucleic acid, are used to stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is an epitope or peptide derived from one of the prostate specific proteins of the invention. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.uspto.gov/sequence.html?DocID=20030185830.
 XX Sequence 19 AA:
 Query Match 100.0%; Score 106; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; OS

Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 1 GFTNYTDFEDSPYFKENSA 19
 RESULT 8
 ADG26370 standard; peptide; 19 AA.
 AC ADG26370;
 DT 26-FEB-2004 (first entry)
 XX Human prostate-specific polypeptide #43.
 DE Human prostate-specific polypeptide; prostate cancer; cytostatic.
 XX Homo sapiens.

XX PN US2003157089-A1.
 XX PD 21-AUG-2003.
 XX PF 09-MAY-2002; 2002US-00144678.
 XX PR 25-FEB-1997; 97US-0086099.
 XX PR 01-AUG-1997; 97US-0094804.
 XX PR 09-FEB-1998; 98US-0000956.
 XX PR 14-JUL-1998; 98US-00010607.
 XX PR 23-SEP-1998; 98US-00159812.
 XX PR 09-APR-1999; 99US-00212149.
 XX PR 13-UTL-1999; 99US-0032946.
 XX PR 12-NOV-1999; 99US-00439313.
 XX PR 18-NOV-1999; 99US-00433686.
 XX PR 14-JAN-2000; 2000US-00433672.
 XX PR 27-MAR-2000; 2000US-00516857.
 XX PR 09-MAY-2000; 2000US-00588100.
 XX PR 12-MAY-2000; 2000US-0057037.
 XX PR 13-JUN-2000; 2000US-0053793.
 XX PR 27-JUN-2000; 2000US-0065783.
 XX PR 09-AUG-2000; 2000US-00636215.
 XX PR 29-AUG-2000; 2000US-0061236.
 XX PR 06-SEP-2000; 2000US-0067279.
 XX PR 02-OCT-2000; 2000US-00679426.
 XX PR 10-OCT-2000; 2000US-0065166.
 XX PR 09-NOV-2000; 2000US-00709729.
 XX PR 12-JAN-2001; 2001US-00759143.
 XX PR 09-FEB-2001; 2001US-0070669.
 XX PR 09-MAY-2001; 2001US-0082911.
 XX PR 29-JUN-2001; 2001US-00895814.
 XX PR 10-DEC-2001; 2001US-00012896.
 XX DR WPI: 2003-777973/73.
 XX New polynucleotides encoding prostate specific polypeptides isolated from a human prostate tumor cDNA library are useful to diagnose and treat cancer particularly prostate cancer.
 XX PA (CORI-X) CORIXA CORP.
 XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SJ, Jiang Y, Henderson RA, Kalsi MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedrick TS, Carrier D, Li SX, Wang A, Skeirly YAN, Hepler WT, Hural J; McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y, Meagher MJ, Deng T;
 XX DR WPI: 2003-777973/73.
 XX New polynucleotides encoding prostate specific polypeptides isolated from a human prostate tumor cDNA library are useful to diagnose and treat cancer particularly prostate cancer.
 XX PS Example 18; SEQ ID NO 504; 99pp; English.
 XX The invention relates to human prostate-specific polypeptides and the polynucleotides encoding them. The invention also relates to an isolated polypeptide or its antigen-binding fragment that specifically binds a polypeptide of the invention, a method of detecting cancer in a patient comprising contacting a biological sample of the patient with an agent that binds a prostate-specific polypeptide and comparing the amount of bound polypeptide compared to a predetermined cut-off value and a fusion protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate cancer. This sequence represents a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX SQ Sequence 19 AA:
 XX Query Match 100.0%; Score 106; DB 7; Length 19;
 XX Best Local Similarity 100.0%; Pred. No. 6.2e-09; Mismatches 0; Indels 0; Gaps 0;
 XX Matches 19; Conservative 0; OS
 Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 1 GFTNYTDFEDSPYFKENSA 19
 RESULT 8
 ADG26370 standard; peptide; 19 AA.
 AC ADG26370;
 DT 26-FEB-2004 (first entry)
 XX Human prostate-specific polypeptide #43.
 DE Human prostate-specific polypeptide; prostate cancer; cytostatic.
 XX Homo sapiens.

Query Match 100.0%; Score 106; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; OS

| | | | |
|--|--|--|----------------------------|
| REVIEW 9 | | QY | 1 GFTNTTDFFDSFYFKENSA 19 |
| RESULT 9 | ADD69590 standard; protein; 172 AA. | Db | 82 GFTNTTDFFDSFYFKENSA 100 |
| SID XX | XX | RESULT 10 | ADP81123 |
| ADD69590; | XX | ID ADP81123 standard; protein; 174 AA. | XX |
| AC AC | XX | XX | XX |
| AM AC | XX | DE 09-SEP-2004 (First entry) | XX |
| DT DT | XX | DE Protein of human ovarian specific gene, SEQ ID No 157. | XX |
| Human REMAP protein - SEQ ID 19. | XX | KW normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA; metastatic; cancer; vaccine; cytostatic; human. | XX |
| DE | XX | KW | XX |
| human; receptor and membrane-associated protein; REMAP; cytostatic; anti-arteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; cell proliferative; cancer; atherosclerosis; neurological; epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS; allergy; developmental; hypothyroidism; Cushing's syndrome; infection. | XX | KW | XX |
| XX | XX | KW | XX |
| Homo sapiens. | OS | XX | OS |
| PN | XX | XX | Homosapiens. |
| WO2003048305-A2. | XX | XX | XX |
| PD 24-JUN-2004. | XX | PD 24-JUN-2004. | XX |
| XX | XX | XX | XX |
| PP 08-DEC-2003; | XX | PP 08-DEC-2003; | XX |
| PD 12-JUN-2003. | XX | PD 12-JUN-2003. | XX |
| PR 06-DEC-2002; | XX | PR 06-DEC-2002; | XX |
| PF 13-NOV-2002; 2002WO-US036759. | XX | PF 13-NOV-2002; 2002WO-US036759. | XX |
| PR 06-DEC-2002; | XX | PR 06-DEC-2002; | XX |
| PR 13-NOV-2001; 2001US-0333097P. | XX | PR 13-NOV-2001; 2001US-0333097P. | XX |
| PR 3-DEC-2001; 2001US-033574P. | XX | PR 3-DEC-2001; 2001US-033574P. | XX |
| PR 14-DEC-2001; 2001US-034542P. | XX | PR 14-DEC-2001; 2001US-034542P. | XX |
| PR 18-DEC-2001; 2001US-0342166P. | XX | PR 18-DEC-2001; 2001US-0342166P. | XX |
| PR 11-JAN-2002; 2002US-0347580P. | XX | PR 11-JAN-2002; 2002US-0347580P. | XX |
| PR 14-JAN-2002; 2002US-0348687P. | XX | PR 14-JAN-2002; 2002US-0348687P. | XX |
| (INCY-) INCYTE GENOMICS INC. | XX | WPI: 2004-46850/44. | XX |
| PA DR N-PSDB; ADP80988. | XX | DR N-PSDB; ADP80988. | XX |
| CC New ovarian specific nucleic acid molecules and polypeptides useful for diagnosing, preventing or treating ovarian cancer, for producing transgenic animals or cells, or for research purposes. | XX | CC New ovarian specific nucleic acid molecules and polypeptides useful for diagnosing, preventing or treating ovarian cancer, for producing transgenic animals or cells, or for research purposes. | XX |
| CC Claim 12; SEQ ID NO 157; 754pp; English. | XX | CC Claim 12; SEQ ID NO 157; 754pp; English. | XX |
| CC The invention relates to novel isolated nucleic acid molecules and polypeptides present in normal and neoplastic ovarian cells. These polypeptides comprise a nucleic acid sequence encoding any of the 167 amino acid sequences (e.g. 438', 237 or 233 amino acids) fully defined in the specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention further comprises: a method for determining the presence of a ovarian specific nucleic acid (OSNA) in a sample; a vector comprising the above nucleic acid molecule; a host cell comprising the vector; a method for producing a polypeptide encoded by the above nucleic acid molecule; a polypeptide encoded by the nucleic acid molecule cited above; an antibody or its fragment that specifically binds to the above polypeptide; a method for determining the presence of an ovarian specific protein in a sample; a method for diagnosing or monitoring the presence and metastases of ovarian cancer in a patient, the kit for detecting a risk of cancer or presence of cancer in a patient, the kit comprising a means for determining the presence of the above nucleic acid molecule or polypeptide; a method of treating a patient with ovarian cancer; and a vaccine comprising the above polypeptide or nucleic acid encoding the polypeptide. The isolated nucleic acid molecules and polypeptides have cytostatic activity. The isolated polypeptides may be used to create a vaccine. The isolated nucleic acid molecules and polypeptides can be used for diagnosing or monitoring the presence and metastases of ovarian cancer and treating ovarian cancer. This sequence represents the protein sequence 172 AA; | CC Sequence 172 AA; | | |
| CC Query Match 100.0%; Score 106; DB 7; Length 172; | CC Best Local Similarity 100.0%; Pred. No. 6-78; | | |
| CC Matches 0; Mismatches 0; Indels 0; Gaps 0; | CC SQ Sequence 174 AA; | | |

weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR6505-ADR6654 represent the invention.

XX Sequence 214 AA;
 SQ Query Match 100.0%; Score 106; DB 8; Length 214;
 Best Local Similarity 100.0%; Pred. No. 8.5e-08; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;
 QY 1 GFTNYTDFEDSPYFKNSA 19
 Db 124 GFTNYTDFEDSPYFKNSA 142

RESUIT 13
 AAW75060
 ID AAW75060 standard; protein; 233 AA.
 XX AC AAW75060;
 XX DT 25-MAR-2003 (revised)
 DT 28-JAN-1999 (first entry)
 DE Human secreted protein encoded by gene 4 clone HKCSR70.
 XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 KW
 XX Homo sapiens.
 XX Key Location/Qualifiers
 PH Misc-difference 233
 FT /label= unknown

FT
 OS WO983946-A2.
 PN XX
 FD 11-SEP-1998.
 PR 06-MAR-1998; 98WO-US004482.
 XX
 PR 07-MAR-1997; 97US-0038621P.
 PR 07-MAR-1997; 97US-0040161P.
 PR 07-MAR-1997; 97US-0040162P.
 PR 07-MAR-1997; 97US-004163P.
 PR 07-MAR-1997; 97US-0040333P.
 PR 07-MAR-1997; 97US-0040334P.
 PR 07-MAR-1997; 97US-0040622P.
 PR 11-APR-1997; 97US-0043311P.
 PR PR 11-APR-1997; 97US-0043313P.
 PR PR 11-APR-1997; 97US-0043314P.
 PR PR 11-APR-1997; 97US-0043315P.
 PR PR 11-APR-1997; 97US-0043568P.
 PR PR 11-APR-1997; 97US-0043576P.
 PR PR 11-APR-1997; 97US-0043578P.
 PR PR 11-APR-1997; 97US-0043580P.
 PR PR 11-APR-1997; 97US-0043669P.
 PR PR 11-APR-1997; 97US-0043670P.
 PR PR 11-APR-1997; 97US-0043671P.
 PR PR 11-APR-1997; 97US-0043672P.
 PR PR 11-APR-1997; 97US-0043674P.
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 PR PR 11-APR-1997; 97US-0044750P.
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 PR PR 11-APR-1997; 97US-00447502P.
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 PR PR 11-APR-1997; 97US-00447581P.
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 PR PR 11-APR-1997; 97US-00447583P.
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 PR PR 11-APR-1997; 97US-00447586P.
 PR PR 11-APR-1997; 97US-00447587P.
 PR PR 11-APR-1997; 97US-00447588P.
 PR PR 11-APR-1997; 97US-00447589P.
 PR PR 11-APR-1997; 97US-00447590P.
 PR PR 11-APR-1997; 97US-00447592P.
 PR PR 11-APR-1997; 97US-00447593P.
 PR PR 11-APR-1997; 97US-00447594P.
 PR PR 11-APR-1997; 97US-00447595P.
 PR PR 11-APR-1997; 97US-00447596P.
 PR PR 11-APR-1997; 97US-00447597P.
 PR PR 11-APR-1997; 97US-00447598P.
 PR PR 11-APR-1997; 97US-00447599P.
 PR PR 11-APR-1997; 97US-00447600P.
 PR PR 11-APR-1997; 97US-00447601P.
 PR PR 11-APR-1997; 97US-00447612P.
 PR PR 11-APR-1997; 97US-00447613P.
 PR PR 11-APR-1997; 97US-00447614P.
 PR PR 11-APR-1997; 97US-00447615P.
 PR PR 11-APR-1997; 97US-00447617P.
 PR PR 11-APR-1997; 97US-00447618P.
 PR PR 11-APR-1997; 97US-00447622P.
 PR PR 11-APR-1997; 97US-00447633P.
 PR PR 06-JUN-1997; 97US-0044894P.
 PR PR 06-JUN-1997; 97US-0044894P.
 PR PR 22-AUG-1997; 97US-0056530P.
 PR PR 22-AUG-1997; 97US-0056531P.
 PR PR 22-AUG-1997; 97US-0056532P.
 PR PR 22-AUG-1997; 97US-0056536P.
 PR PR 22-AUG-1997; 97US-0056537P.
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 PR PR 22-AUG-1997; 97US-0056539P.
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 PR PR 22-AUG-1997; 97US-0056541P.
 PR PR 22-AUG-1997; 97US-0056542P.
 PR PR 22-AUG-1997; 97US-0056546P.
 PR PR 22-AUG-1997; 97US-0056547P.
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 PR PR 22-AUG-1997; 97US-0056549P.
 PR PR 22-AUG-1997; 97US-0056550P.
 PR PR 22-AUG-1997; 97US-0056551P.
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 PR PR 22-AUG-1997; 97US-0056553P.
 PR PR 22-AUG-1997; 97US-0056554P.
 PR PR 22-AUG-1997; 97US-0056555P.
 PR PR 22-AUG-1997; 97US-0056556P.
 PR PR 22-AUG-1997; 97US-0056557P.
 PR PR 22-AUG-1997; 97US-0056558P.
 PR PR 22-AUG-1997; 97US-0056559P.
 PR PR 22-AUG-1997; 97US-0056560P.
 PR PR 22-AUG-1997; 97US-0056561P.
 PR PR 22-AUG-1997; 97US-0056562P.
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 PR PR 22-AUG-1997; 97US-0056564P.
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 PR PR 22-AUG-1997; 97US-0056587P.
 PR PR 22-AUG-1997; 97US-0056588P.
 PR PR 22-AUG-1997; 97US-0056589P.
 PR PR 22-AUG-1997; 97US-0056590P.

| | |
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| KW | head trauma; stroke; tissue regeneration; congenital defect; trauma; |
| PR | 22-AUG-1997; 97US-0056889P. |
| PR | 22-AUG-1997; 97US-0056892P. |
| PR | 22-AUG-1997; 97US-0056893P. |
| PR | 22-AUG-1997; 97US-0056894P. |
| PR | 22-AUG-1997; 97US-0056903P. |
| PR | 22-AUG-1997; 97US-0056908P. |
| PR | 22-AUG-1997; 97US-0056909P. |
| PR | 22-AUG-1997; 97US-0056910P. |
| PR | 22-AUG-1997; 97US-0056911P. |
| PR | 05-SEP-1997; 97US-0057650P. |
| PR | 05-SEP-1997; 97US-0057761P. |
| XX | (HUMA-) HUMAN GENOME SCI INC. |
| XX | PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC; PI Bednarzik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM; PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA; PI Moore PA, Shi Y, Lafleur DW, Lii Y, Zeng Z, Kyaw H; |
| XX | DR WPI; 1998-609887/51. |
| XX | PT New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders. |
| XX | PS Claim 1; Page 281-282; 447pp; English. |
| XX | CC This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV34145) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 70 novel genes and their fragments (nucleic acid sequences: AAV34145-V34276; amino acid sequences AAV34057-W37179) which are useful for preventing, treating or ameliorating medical conditions by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 70 polynucleotides, based on which tissues they are most highly expressed in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct CC PF field.) (Updated on 25-MAR-2003 to correct PI field.) |
| XX | SQ Sequence 233 AA; |
| Qy | Query Match 100.0%; Score 106; DB 2; Length 233; Best Local Similarity 100.0%; Pred. No. 9_3e-08; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Db | 1 GFTNYTDFEDSPYFKENSA 19 142 GFTNYTDFEDSPYFKENSA 160 |
| RESULT 14 | ABO01936 Novel 1 human secreted protein #4. |
| ID | ABO01936 standard; protein; 233 AA. |
| XX | AC ABO01936; |
| XX | DT 12-AUG-2003 (first entry) |
| DE | Novel 1 human secreted protein #4. |
| XX | Human; immunoglobulin G; IgG; fragment of crystallisation; FC; immune system disorder; haematopoietic cell disorder; HIV infection; immunologic deficiency disorder; ataxia telangiectasia; HIV infection; Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria; blood coagulation disorder; blood Platelet disorder; autoimmune disorder; Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis; glomerulonephritis; Grave's disease; allergic reaction; hyperproliferative disorder; neoplasm; graft-versus-host disease; hyperplastic disorder; spinal cord disorder; infectious disease; nervous system disease; 97US-0048974P; 97US-0056630P; 97US-0056631P; KW |

| | | | | |
|----|--------------|----------------|--------------------|--|
| PR | 22-AUG-1997; | 97US-0056632P. | CC | (PS) fully defined in the specification and having biological activity, |
| PR | 22-AUG-1997; | 97US-0056636P. | CC | polypeptide domain or epitope of PS, secreted form of PS, full-length protein of PS, or variant, allelic variant or species homologue of PS. |
| PR | 22-AUG-1997; | 97US-0056637P. | CC | (I) or a polynucleotide (II) encoding (I) is useful for preventing, (I) |
| PR | 22-AUG-1997; | 97US-0056638P. | CC | treating, or ameliorating a medical condition in a mammalian subject. (I) |
| PR | 22-AUG-1997; | 97US-0056664P. | CC | or (II) is also useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject. (I) is useful |
| PR | 22-AUG-1997; | 97US-0056845P. | CC | for identifying a binding partner which involves contacting the |
| PR | 22-AUG-1997; | 97US-0056862P. | CC | partner and determining whether the binding |
| PR | 22-AUG-1997; | 97US-0056864P. | CC | polypeptide with the binding partner and determining whether the binding |
| PR | 22-AUG-1997; | 97US-0056872P. | CC | partner affects the activity of the polypeptide. (I) or (II) is useful |
| PR | 22-AUG-1997; | 97US-0056874P. | CC | for diagnosing or treating deficiencies or disorders of the immune |
| PR | 22-AUG-1997; | 97US-0056875P. | CC | system, deficiencies or disorders of haematopoietic cells, to treat |
| PR | 22-AUG-1997; | 97US-0056876P. | CC | immunologic deficiency disorders, ataxia telangiectasia, HIV infection, |
| PR | 22-AUG-1997; | 97US-0056877P. | CC | Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood |
| PR | 22-AUG-1997; | 97US-0056878P. | CC | coagulation disorders, blood platelet disorders, autoimmune disorders |
| PR | 22-AUG-1997; | 97US-0056880D. | CC | (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis, |
| PR | 22-AUG-1997; | 97US-0056881P. | CC | dermatitis glomerulonephritis, Grave's disease), allergic reactions |
| PR | 22-AUG-1997; | 97US-0056882P. | CC | graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms |
| PR | 22-AUG-1997; | 97US-0056884P. | CC | located in the abdomen, bone, breast, digestive system, liver, pancreas, |
| PR | 22-AUG-1997; | 97US-0056886P. | CC | peritoneum, endocrine glands, infectious diseases (e.g., viral, |
| PR | 22-AUG-1997; | 97US-0056887P. | CC | bacterial, fungal or parasitic infection), central and peripheral nervous |
| PR | 22-AUG-1997; | 97US-0056888P. | CC | system diseases (e.g., spinal cord disorders, head trauma or stroke), to |
| PR | 22-AUG-1997; | 97US-0056889P. | CC | differentiate, proliferate and attract cells leading to the regeneration |
| PR | 22-AUG-1997; | 97US-0056890P. | CC | of tissues to repair, replace or protect tissue damaged by congenital |
| PR | 22-AUG-1997; | 97US-0056892P. | CC | defects, trauma (wounds, burns, incisions or ulcers), age disease (e.g., |
| PR | 22-AUG-1997; | 97US-0056893P. | CC | osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV) |
| PR | 22-AUG-1997; | 97US-0056894P. | CC | is useful to modulate mammalian characteristics, to modulate mammalian |
| PR | 22-AUG-1997; | 97US-0056903P. | CC | metabolism affecting catabolism, anabolism, processing, utilisation, and |
| PR | 22-AUG-1997; | 97US-0056908P. | CC | storage of energy, to change a mammal's mental state or physical state, |
| PR | 22-AUG-1997; | 97US-0056909P. | CC | or as a food additive or preservative, such as to increase or decrease |
| PR | 22-AUG-1997; | 97US-0056910P. | CC | storage capabilities, fat content, lipid, protein, carbohydrate, |
| PR | 05-SEP-1997; | 97US-0056911P. | CC | vitamins, minerals, cofactors or other nutritional components. This is |
| PR | 05-SEP-1997; | 97US-0056509P. | CC | the amino acid sequence of a novel human secreted protein |
| PR | 06-MAR-1998; | 98US-004482. | XX | XX Sequence 233 AA; |
| XX | | | Query Match | Score 106; DB 6; |
| | | | Best Local Matches | 19; Consimilarity 100 %; Pred. No. 9.3e-08; |
| | | | | Mismatches 0; Indels 0; Gaps 0; |
| Qy | | | 1 | GFTNYTDFDSFYKNSA 19 |
| Db | | | 142 | GFTNYTDFDSFYKNSA 160 |
| | | | RESULT 15 | |
| | | | ID AAG62153 | |
| | | | XX | XX Human P503S inventive antigen SEQ ID NO: 352. |
| | | | AC | AAG62153; |
| | | | XX | XX |
| | | | DT | 06-JUL-2001 (first entry) |
| | | | XX | XX |
| | | | DB | Human mouse; immunotherapy; cancer; leukaemia; WT1; Wilms' tumour gene; |
| | | | XX | KW chromosome 11p13; zinc finger transcription factor. |
| | | | XX | XX Homo sapiens. |
| | | | PN | WO20015273-A2. |
| | | | XX | XX |
| | | | PD | 12-APR-2001. |
| | | | XX | XX |
| | | | PT | 04-OCT-2000; 2000WO-US027445. |
| | | | XX | XX |
| | | | PR | 04-OCT-1999; 99US-015745P. |
| | | | XX | XX (CORI-) CORIXA CORP. |
| | | | PA | PA Skeiky YAW, Xu J, Cheever MA, Reed SG; |
| | | | XX | XX DR WPI, 2001-326324/34. |
| | | | PT | PT Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing |
| | | | PR | PR or treating deficiencies or disorders of the immune system, autoimmune |
| | | | PT | PT disorders, hyperproliferative disorders, and infectious diseases. |
| | | | XX | XX |
| PS | | | XX | XX Claim 11; Page 173; 243PP; English. |
| | | | XX | XX DR N-PSDB, ACD08028. |
| | | | XX | XX PT Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing |
| | | | PT | PT or treating deficiencies or disorders of the immune system, autoimmune |
| | | | PT | PT disorders, hyperproliferative disorders, and infectious diseases. |
| | | | XX | XX |
| | | | PS | PS The invention describes an isolated human secreted HODAZ50 polypeptide |
| | | | CC | CC (I) comprising a sequence at least 95% identical to a sequence selected |
| | | | CC | CC from polypeptide fragment of any one of the 123 polypeptide sequences |

CX Polypeptide comprising part of the Wilms Tumor gene product sequence is
CPT used in the diagnosis and treatment of malignant diseases e.g. leukemia
CCC and cancer associated with WT1.
CC Disclosure: Page 223-224: 228PP; English.

CC The present invention describes compositions comprising peptides derived
CCC from the Wilm's tumour protein WT1 and methods for their use in treating
CCC malignant diseases. Peptides derived from both the murine and human WT1
CCC proteins are provided. The human WT1 gene is found on chromosome 11p13,
CCC and the protein was shown to be a zinc finger transcription factor. The
CCC immunogenic peptides of the invention are particularly useful in the
CCC diagnosis and treatment of cancer and leukemia. The present sequence is
CCC a polypeptide described in the exemplification of the invention

| Sequence 240 AA: | | | | | | |
|------------------|--------------------------------------|----------------------------|-----------------------------|-----------------------------|------------------------------|---------------------|
| | Query Match Best Local Matches | Match Similarity 19; | Score 100.0%; 100.0%; | DB 4; Pred. No. 9.6e-08; | Length 240; Mismatches 0; | Index 0; Gaps 0; |
| Qy | 1 | GFPNYTDPEDSPYKNSA | 19 | | | |
| Ds | 151 | GFPNYTDPEDSPYKNSA | 169 | | | |

Search completed: February 5, 2005, 19:59:55
Job time : 100 508 secs

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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:50:20 ; Search time 24.1525 Seconds
(without alignments)
58.724 Million cell updates/sec

Title: US-09-780-669-114_COPY_151_169
Perfect score: 106
Sequence: 1 GFTNYTDFDSPYFKENSA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

| Database : | Issued Patents AA:* | | | | | | | | | | |
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| 2: | /cgn2_6/prodata/1/iaa/5B_COMB.pep:* | | | | | | | | | | |
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| 5: | /cgn2_6/prodata/1/iaa/PC705_COMB.pep:* | | | | | | | | | | |
| 6: | /cgn2_6/prodata/1/iaa/backfiles1.pep:* | | | | | | | | | | |
| Pred. No. | is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | | | | | |
| SUMMARIES | | | | | | | | | | | |
| Result No. | Score | Query Match | Length | DB ID | Description | | | | | | |
| 1 | 106 | 100.0 | 19 | 3 US-09-439-313-504 | Sequence 504, APP | | | | | | |
| 2 | 106 | 100.0 | 19 | 4 US-09-636-215-504 | Sequence 504, APP | | | | | | |
| 3 | 106 | 100.0 | 19 | 4 US-09-685-106A-504 | Sequence 504, APP | | | | | | |
| 4 | 106 | 100.0 | 19 | 4 US-09-679-426-504 | Sequence 504, APP | | | | | | |
| 5 | 106 | 100.0 | 19 | 4 US-09-759-143-504 | Sequence 504, APP | | | | | | |
| 6 | 106 | 100.0 | 19 | 4 US-09-226-504 | Sequence 504, APP | | | | | | |
| 7 | 106 | 100.0 | 233 | 4 US-09-148-545-137 | Sequence 137, APP | | | | | | |
| 8 | 106 | 100.0 | 241 | 3 US-08-808-148-1 | Sequence 1, APP | | | | | | |
| 9 | 106 | 100.0 | 241 | 3 US-09-926-114 | Sequence 114, APP | | | | | | |
| 10 | 106 | 100.0 | 241 | 3 US-09-030-607-114 | Sequence 114, APP | | | | | | |
| 11 | 106 | 100.0 | 241 | 3 US-09-339-313-114 | Sequence 114, APP | | | | | | |
| 12 | 106 | 100.0 | 241 | 3 US-09-352-616A-114 | Sequence 114, APP | | | | | | |
| 13 | 106 | 100.0 | 241 | 4 US-09-132-149A-114 | Sequence 114, APP | | | | | | |
| 14 | 106 | 100.0 | 241 | 4 US-09-159-812-114 | Sequence 114, APP | | | | | | |
| 15 | 106 | 100.0 | 241 | 4 US-09-336-215-114 | Sequence 114, APP | | | | | | |
| 16 | 106 | 100.0 | 241 | 4 US-09-685-166A-114 | Sequence 114, APP | | | | | | |
| 17 | 106 | 100.0 | 241 | 4 US-09-115-453-114 | Sequence 114, APP | | | | | | |
| 18 | 106 | 100.0 | 241 | 4 US-09-388-489-114 | Sequence 114, APP | | | | | | |
| 19 | 106 | 100.0 | 241 | 4 US-09-679-416-114 | Sequence 114, APP | | | | | | |
| 20 | 106 | 100.0 | 241 | 4 US-09-579-143-114 | Sequence 114, APP | | | | | | |
| 21 | 106 | 100.0 | 241 | 4 US-09-651-226-114 | Sequence 114, APP | | | | | | |
| 22 | 87 | 82.1 | 43 | 4 US-09-663-600A-123 | Sequence 123, APP | | | | | | |
| 23 | 87 | 82.1 | 43 | 4 US-09-663-600A-223 | Sequence 223, APP | | | | | | |
| 24 | 51 | 48.1 | 249 | 4 US-09-949-016-8334 | Sequence 8334, APP | | | | | | |
| 25 | 49 | 46.2 | 252 | 4 US-09-870-771-17 | Sequence 17, APP | | | | | | |
| 26 | 49 | 46.2 | 252 | 4 US-09-117-540-17 | Sequence 17, APP | | | | | | |
| 27 | 42.5 | 42.5 | 223 | 4 US-09-270-767-61548 | Sequence 61548, A | | | | | | |

ALIGNMENTS

RESULT 1
US-09-439-313-504
; Sequence 504, Application US/09439313
; Patent No. 6329505

GENERAL INFORMATION:
 / APPLICANT: XU, Jiangchun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan Louise
 / APPLICANT: Jiang, Yuqiu
 / APPLICANT: Reed, Steven G.
 / APPLICANT: Kalos, Michael J.
 / APPLICANT: Fanger, Gary
 / APPLICANT: Retter, Mark
 / APPLICANT: Solt, John
 / APPLICANT: Day, Craig
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 / TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 / FILE REFERENCE: 2101214.427C9
 / CURRENT APPLICATION NUMBER: US/09/419,313
 / CURRENT FILING DATE: 1999-11-12
 / NUMBER OF SEQ ID NO: 575

SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO 504
 / LENGTH: 19
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Made in a lab
 / US-09-439-313-504

Query Match 100.0%; Score 106; DB 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFDSPYFKENSA 19
 Db 1 GFTNYTDFDSPYFKENSA 19

RESULT 2
US-09-636-215-504
; Sequence 504, Application US/09636215
; Patent No. 6620922

GENERAL INFORMATION:
 / APPLICANT: XU, Jiangchun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan Louise
 / APPLICANT: Jiang, Yuqiu

APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 Fanger, Gary R.
 Reitter, Marc W.
 APPLICANT: Shrolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 APPLICANT: Title of Invention: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121 42717C17
 CURRENT APPLICATION NUMBER: US/09/636,215
 CURRENT FILING DATE: 2000-08-10
 NUMBER OF SEQ ID NOS: 852
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 504
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFNTNYTDFEDSPYFKNSA 19
 Db 1 GFNTNYTDFEDSPYFKNSA 19

RESULT 3
 US-09-685-166A-504
 Sequence 504, Application US/09685166A
 Patent No. 6630305
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlicker, Susan L.
 APPLICANT: Jiang, Yuqiu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Reitter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121 427C21
 CURRENT APPLICATION NUMBER: US/09/685,166A
 CURRENT FILING DATE: 2000-10-10
 NUMBER OF SEQ ID NOS: 898
 SEQ ID NO: 504
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

US-09-685-166A-504
 Sequence 504, Application US/09685166A
 Patent No. 6630305
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlicker, Susan L.
 APPLICANT: Jiang, Yuqiu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Reitter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick

Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFNTNYTDFEDSPYFKNSA 19
 Db 1 GFNTNYTDFEDSPYFKNSA 19

RESULT 4
 US-09-679-426-504
 Sequence 504, Application US/09679426
 Patent No. 6759515
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlicker, Susan L.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Reitter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlicker, Susan L.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Reitter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick

Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFNTNYTDFEDSPYFKNSA 19
 Db 1 GFNTNYTDFEDSPYFKNSA 19

RESULT 5
 US-09-759-143-504
 Sequence 504, Application US/09759143
 Patent No. 6800746
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlicker, Susan L.
 APPLICANT: Jiang, Yuqiu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Reitter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121_427C23
 CURRENT APPLICATION NUMBER: US/09/759_143
 CURRENT FILING DATE: 2001-01-12
 NUMBER OF SEQ ID NOS: 934
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 504
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNTYDFFEDSPYFKNSA 19
 Db 1 GFTNTYDFFEDSPYFKNSA 19

RESULT 6
 US-09-651-236-504
 Sequence 504, Application US/09651236
 GENERAL INFORMATION:
 Patent No. 6818751

APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugui
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Derrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121_427C18
 CURRENT APPLICATION NUMBER: US/09/651_236
 CURRENT FILING DATE: 2000-08-29
 NUMBER OF SEQ ID NOS: 865
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 504
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

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; ; EARLIER FILING DATE: 1997-04-11
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; ; EARLIER FILING DATE: 1997-08-22
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; ; EARLIER FILING DATE: 1997-08-22
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; ; EARLIER APPLICATION NUMBER: 60/056,845
; ; EARLIER FILING DATE: 1997-08-22
; ; EARLIER APPLICATION NUMBER: 60/056,892
; ; EARLIER FILING DATE: 1997-08-22
; ; EARLIER APPLICATION NUMBER: 60/047,595
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; ; EARLIER APPLICATION NUMBER: 60/047,594
; ; EARLIER FILING DATE: 1997-05-23
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; ; EARLIER FILING DATE: 1997-05-23
; ; EARLIER APPLICATION NUMBER: 60/047,593
; ; EARLIER FILING DATE: 1997-05-23
; ; EARLIER APPLICATION NUMBER: 60/047,614
; ; EARLIER FILING DATE: 1997-05-23
; ; EARLIER APPLICATION NUMBER: 60/043,578
; ; EARLIER FILING DATE: 1997-04-11
; ; EARLIER APPLICATION NUMBER: 60/043,576
; ; EARLIER FILING DATE: 1997-04-11
; ; EARLIER APPLICATION NUMBER: 60/047,501
; ; EARLIER FILING DATE: 1997-05-23
; ; EARLIER APPLICATION NUMBER: 60/043,670
; ; EARLIER FILING DATE: 1997-04-11
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; ; EARLIER APPLICATION NUMBER: 60/043,676
; ; EARLIER FILING DATE: 1997-08-22
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; ; EARLIER FILING DATE: 1997-08-22
; ; EARLIER APPLICATION NUMBER: 60/048,964
; ; EARLIER FILING DATE: 1997-06-06
; ; EARLIER APPLICATION NUMBER: 60/057,650
; ; EARLIER FILING DATE: 1997-09-05
; ; EARLIER APPLICATION NUMBER: 60/056,844
; ; EARLIER FILING DATE: 1997-08-22
; ; NUMBER OF SEQ ID NOS: 280
; ; SOFTWARE: PatentIn Ver. 2.0
; ; SEQ ID NO: 137
; ; LENGTH: 233
Query Match          100.0%; Score 106; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;
Qy      1 GFTNYTDFDSPYFKENSA 19
Db      142 GFTNYTDFDSPYFKENSA 160
RESULT 8
US-08-808-148-1
; Sequence 1, Application US/08808148
; Patent No. 6020478
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer
;
```

APPLICANT: Goli, Surya
 APPLICANT: Zhang, Hong Wolfe
 TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ FOR Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/808,148
 FILING DATE: Herewith
 CLASIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PR-0218 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-0555
 TELEX:
 TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

IMMEDIATE SOURCE:

PROSNOR26

CLONE: 2187263

US-08-808-148-1

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

IMMEDIATE SOURCE:

PROSNOR26

CLONE: 2187263

US-08-808-148-1

RESULT 10

US-09-030-607-114

; Sequence 114, Application US/09030607

; Patent No. 626225

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO

; NUMBER OF SEQUENCES: 224

; CORRESPONDENCE ADDRESS:

; ADDRESSE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIPP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/030,607

; FILING DATE: 25-FEB-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; INFORMATION FOR SEQ ID NO: 114:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 241 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; US-09-030-607-114

RESULT 9

US-09-020-956-114

; Sequence 114, Application US/09020956

; Patent No. 6261562

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO

; NUMBER OF SEQUENCES: 178

; CORRESPONDENCE ADDRESS:

; ADDRESSE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIPP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

Query Match, Similarity 100.0%; Score 106; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 13
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 ; Sequence 114, Application US/09232149A.
 ; Patent No. 6465611.
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
 ; FILE REFERENCE: 210121.42766
 ; CURRENT APPLICATION NUMBER: US/09/232,149A
 ; CURRENT FILING DATE: 1999-01-15
 ; NUMBER OF SEQ ID NOS: 338
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 114
 ; LENGTH: 241
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-232-149A-114

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 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GFTNYTDFDSFYKNSA 19
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RESULT 14
 US-09-159-812-114
 ; Sequence 114, Application US/09159812A.
 ; Patent No. 6613872.
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
 ; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.42825
 ; CURRENT APPLICATION NUMBER: US/09/159,812A
 ; CURRENT FILING DATE: 1998-09-23
 ; NUMBER OF SEQ ID NOS: 306
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 114
 ; LENGTH: 241
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 ; ORGANISM: Homo sapien
 US-09-159-812-114

Query Match, Similarity 100.0%; Score 106; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GFTNYTDFDSFYKNSA 19
 Db 151 GFTNYTDFDSFYKNSA 169

RESULT 12
 US-09-352-616A-114
 ; Sequence 114, Application US/09352616A.
 ; Patent No. 6395278.
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Harlock, Susan Louise
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.427C8
 ; CURRENT APPLICATION NUMBER: US/09/352,616A
 ; CURRENT FILING DATE: 1999-07-13
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 ; LENGTH: 241
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 ; ORGANISM: Homo sapien
 US-09-352-616A-114

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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GFTNYTDFDSFYKNSA 19
 Db 151 GFTNYTDFDSFYKNSA 169

RESULT 15
 US-09-536-215-114
 ; Sequence 114, Application US/09636215.
 ; Patent No. 6620922.
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121_42717C17
; CURRENT APPLICATION NUMBER: US/09/635,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
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; SEQ ID NO 114
; LENGTH: 241
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; ORGANISM: Homo sapien
us-09-636-215-114

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Job time : 25.1525 secs

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OM protein - protein search, using SW model

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RESULT 1
US-09-759-143-504

Sequence 504, Application US/09759143

Patent No. US2003022248A1

GENERAL INFORMATION:

XU, Jiangchun

Dillon, Davin C.

Mitcham, Jennifer L.

Harlocker, Susan L.

Jiang, Yuqui

Henderson, Robert A.

Kaios, Michael D.

Panger, Gary R.

Retter, Marc W.

Stolk, John A.

Day, Craig H.

Vedick, Thomas S.

Carter, Darrick

Li, Samuel

Wang, Ajun

Skeky, Yasir A.W.

Applicant: Stolk, John A.

Applicant: Day, Craig H.

Applicant: Vedick, Thomas S.

Applicant: Carter, Darrick

Applicant: Li, Samuel

Applicant: Wang, Ajun

Applicant: Skeky, Yasir A.W.

Applicant: Hepler, William

Title of Invention: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121-427C3

Title of Invention: DIAGNOSIS OF PROSTATE CANCER

Current Application Number: US/09/759,143

Current Filing Date: 2001-01-12

Number of SEQ ID NOS: 934

Software: FastSEQ For Windows Version 3.0

SEQ ID NO 504

Length: 19

Type: PRT

Organism: Artificial Sequence

Feature:

Other Information: Made in a lab

US-09-759-143-504

SUMMARIES

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| 2 | 106 | 100.0 | 19 | 9 US-09-780-669-114 | Sequence 504, App |
| 3 | 106 | 100.0 | 19 | 9 US-09-822-827-114 | Sequence 504, App |
| 4 | 106 | 100.0 | 19 | 9 US-09-115-153-114 | Sequence 504, App |
| 5 | 106 | 100.0 | 19 | 9 US-09-232-380-114 | Sequence 504, App |
| 6 | 106 | 100.0 | 19 | 13 US-09-908-193-44 | Sequence 504, App |
| 7 | 106 | 100.0 | 19 | 13 US-09-895-79-114 | Sequence 504, App |
| 8 | 106 | 100.0 | 19 | 14 US-10-144-678A-504 | Sequence 504, App |
| 9 | 106 | 100.0 | 19 | 14 US-10-144-678A-504 | Sequence 504, App |
| 10 | 106 | 100.0 | 233 | 9 US-09-981-876-117 | Sequence 137, App |
| 11 | 106 | 100.0 | 233 | 10 US-09-148-545-137 | Sequence 137, App |
| 12 | 106 | 100.0 | 240 | 15 US-10-264-37-1489 | Sequence 149, App |
| 13 | 106 | 100.0 | 241 | 9 US-09-759-143-114 | Sequence 114, App |

ALIGNMENTS

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 1 GFTNYTDFEDSPYFKENSA 19

OTHER INFORMATION:
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yuqiu
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Fanger, Gary R.
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedwick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Li, Samuel
 / APPLICANT: Wang, Ajun
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Hepler, William D.
 / APPLICANT: Hural, John
 / APPLICANT: McNeill, Patricia D.
 / APPLICANT: Houghton, Raymond L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121_427C24

CURRENT APPLICATION NUMBER: US/09/780,669

CURRENT FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 943

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 504

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Made in a lab

US-09-780-669-504

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 1 GFTNYTDFEDSPYFKENSA 19

OTHER INFORMATION:
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121_534C2

CURRENT APPLICATION NUMBER: US/09/895,793

CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 504

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Made in a lab

US-09-895-793-504

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 1 GFTNYTDFEDSPYFKENSA 19

OTHER INFORMATION:
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121_534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 504

RESULT 3
 US-09-822-827-504

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 1 GFTNYTDFEDSPYFKENSA 19

OTHER INFORMATION:
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121_534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 504

RESULT 4
 US-09-895-793-504

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 1 GFTNYTDFEDSPYFKENSA 19

OTHER INFORMATION:
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / Publication No. US2002019273A1
 / APPLICANT: Mitcham, Davin C.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yuqiu
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedwick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Li, Samuel X.
 / APPLICANT: Wang, Ajun
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Hepler, William T.
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Hural, John
 / APPLICANT: McNeill, Patricia D.
 / APPLICANT: Houghton, Raymond L.
 / APPLICANT: Vinal de Bassols, Carlota
 / APPLICANT: Foy, Teresa
 / APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121_534C2

CURRENT APPLICATION NUMBER: US/09/895,793

CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 504

RESULT 5
 US-09-895-814-504

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 1 GFTNYTDFEDSPYFKENSA 19

OTHER INFORMATION:
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / Publication No. US20020193296A1
 / APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuguil
 APPLICANT: Katos, Michael D.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Ajun
 APPLICANT: Vinals de Bassols, Carlota
 APPLICANT: Poy, Teresa
 APPLICANT: Fanger, Gary R.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121-427C26
 CURRENT APPLICATION NUMBER: US/09/895,814
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 990
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 504
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

RESULT 6
 US-10-012-896-504
 / Sequence 504, Application US/10012896
 / Publication No. US20020183251A1
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jangchun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yuguil
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Li, Samuel X.
 / APPLICANT: Wang, Ajun
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Heppler, William T.
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Hural, John
 / APPLICANT: McNeill, Patricia D.
 / APPLICANT: Houghton, Raymond L.
 / APPLICANT: Vinals de Bassols, Carlota
 / APPLICANT: Poy, Teresa
 / APPLICANT: Fanger, Gary R.
 / APPLICANT: Wantanabe, Yoshihiro

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 GFTNTDFFDSFYFKENSA 19
 Db 1 GFTNTDFFDSFYFKENSA 19

RESULT 7
 US-10-010-940-504
 / Sequence 504, Application US/10010940
 / Publication No. US20030088062A1
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jangchun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan Louise
 / APPLICANT: Jiang, Yuguil
 / APPLICANT: Reed, Steven G.
 / APPLICANT: Kalos, Michael
 / APPLICANT: Fanger, Gary
 / APPLICANT: Retter, Mark
 / APPLICANT: Soilk, John
 / APPLICANT: Day, Craig
 / APPLICANT: Artificial Sequence
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 / TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 / FILE REFERENCE: 210121-427D3
 / CURRENT APPLICATION NUMBER: US/10/0940
 / CURRENT FILING DATE: 2001-12-05
 / NUMBER OF SEQ ID NOS: 575
 / SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO: 504
 / LENGTH: 19
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Made in a lab

RESULT 8
 US-10-144-678A-504
 / Sequence 504, Application US/10144678A1
 / Publication No. US20030157089A1
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jangchun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yuguil
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Li, Samuel X.
 / APPLICANT: Wang, Ajun
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Heppler, William T.
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Hural, John
 / APPLICANT: McNeill, Patricia D.
 / APPLICANT: Houghton, Raymond L.
 / APPLICANT: Vinals de Bassols, Carlota
 / APPLICANT: Poy, Teresa
 / APPLICANT: Fanger, Gary R.
 / APPLICANT: Wantanabe, Yoshihiro

Query Match 100.0%; Score 106; DB 14; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3 4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Made in a lab
 US-10-144-678A-504

Query Match 100.0%; Score 106; DB 14; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3 4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Made in a lab
 US-10-294-025-504

RESULT 9
 US-09-981-876-137
 / Sequence 137, Application US/09981876
 / Patent No. US2002164669A1
 / GENERAL INFORMATION:
 / APPLICANT: Rosen et al.
 / TITLE OF INVENTION: 70 Human Secreted Proteins
 / FILE REFERENCE: F2001P1
 / CURRENT APPLICATION NUMBER: US/09/981,876
 / CURRENT FILING DATE: 2001-10-19
 / PRIOR APPLICATION NUMBER: 09/148,545
 / PRIOR FILING DATE: 1998-09-04
 / PRIOR APPLICATION NUMBER: 60/040,162
 / PRIOR FILING DATE: 1997-03-07
 / PRIOR APPLICATION NUMBER: 60/040,333
 / PRIOR FILING DATE: 1997-03-07
 / PRIOR APPLICATION NUMBER: 60/039,621
 / PRIOR FILING DATE: 1997-03-07
 / PRIOR APPLICATION NUMBER: 60/040,161
 / PRIOR FILING DATE: 1997-03-07
 / PRIOR APPLICATION NUMBER: 60/040,626
 / PRIOR FILING DATE: 1997-03-07
 / PRIOR APPLICATION NUMBER: 60/040,334
 / PRIOR FILING DATE: 1997-03-07
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 / PRIOR FILING DATE: 1997-05-23
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 / PRIOR APPLICATION NUMBER: 60/047,500
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 / PRIOR FILING DATE: 1997-05-23
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 / PRIOR FILING DATE: 1997-05-23
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 / PRIOR FILING DATE: 1997-05-23
 / PRIOR APPLICATION NUMBER: 60/047,632
 / PRIOR APPLICATION NUMBER: 60/047,632

; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER APPLICATION NUMBER: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER APPLICATION NUMBER: 60/056,886
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; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599

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 EARLIER APPLICATION NUMBER: 60/056,887
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,908
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/048,964
 EARLIER FILING DATE: 1997-06-06
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/056,884
 NUMBER OF SEQ ID NOS: 280
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 137
 LENGTH: 233

Query Match 100.0% Score 106; DB 10; Length 233;
 Best Local Similarity 100.0%; Pred. No. 4.9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

US-10-264-237-1489
 Sequence 1489, Application US/10264237
 Publication No. US20040009491A1
 GENERAL INFORMATION:
 APPLICANT: Birse et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PA131P1
 CURRENT APPLICATION NUMBER: US/10/264,237
 CURRENT FILING DATE: 2002-10-04

; PRIORITY: Application NUMBER: PCT/US01/16450
 ; PRIORITY FILING DATE: 2001-05-18
 ; PRIORITY APPLICATION NUMBER: US 60/205,515
 ; PRIORITY FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 2876
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO: 1489
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-264-237-1489
 Query Match 100.0% Score 106; DB 15; Length 240;
 Best Local Similarity 100.0%; Pred. No. 5.1e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GFTNTYDFEDSPYFKENSA 19
 Db 150 GFTNTYDFEDSPYFKENSA 168
 RESULT 13
 US-09-759-143-114
 Sequence 114, Application US/09759143
 ; Patent No. US2003002248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jianguchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121427C23
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; CURRENT FILING DATE: 2003-01-12
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 114
 ; LENGTH: 241
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-759-143-114
 Query Match 100.0% Score 106; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 5.1e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 US-09-780-669-114
 Sequence 114, Application US/09780669
 ; Patent No. US2003005197A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jianguchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.

i APPLICANT: Harlocker, Susan L.
 i APPLICANT: Jiang, Yugui
 i APPLICANT: Henderson, Robert A.
 i APPLICANT: Kalos, Michael D.
 i APPLICANT: Fainger, Gary R.
 i APPLICANT: Reitter, Marc W.
 i APPLICANT: Stolk, John A.
 i APPLICANT: Day, Craig H.
 i APPLICANT: Vedick, Thomas S.
 i APPLICANT: Carter, Derrick
 i APPLICANT: Li, Samuel
 i APPLICANT: Wang, Ajun
 i APPLICANT: Skeky, Yasir A.W.
 i APPLICANT: Hepler, William
 i APPLICANT: Hural, John
 i APPLICANT: McNeill, Patricia D.
 i APPLICANT: Houghton, Raymond L.
 i TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 i TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 i FILE REFERENCE: 210121 427C2A
 i CURRENT APPLICATION NUMBER: US/09/780,669
 i CURRENT FILING DATE: 2001-02-09
 i NUMBER OF SEQ ID NOS: 943
 i SOFTWARE: FastSEQ For Windows Version 3.0
 i SEQ ID NO: 114
 i LENGTH: 241
 i TYPE: PRT
 i ORGANISM: Homo sapien
 i US-09-780-669-114

Query Match 100.0%; Score 106; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 5.1e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFDSPYFKNSA 19
 Db 151 GFTNYTDFDSPYFKNSA 169

RESULT 15
 US-09-030-606-114
 i Sequence 114, Application US/09030606
 i Patent No. US2002008150A1
 i GENERAL INFORMATION:
 i APPLICANT: Xu, Jiaochun
 i APPLICANT: Dillon, Davin C.
 i TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
 i NUMBER OF SEQUENCES: 224
 i CORRESPONDENCE ADDRESS:
 i ADDRESSEEE: SEED and BERRY LLP
 i STREET: 6300 Columbia Center, 701 Fifth Avenue
 i CITY: Seattle
 i STATE: WA
 i COUNTRY: USA
 i ZIP: 98104
 i COMPUTER READABLE FORM:
 i MEDIUM TYPE: Floppy disk
 i COMPUTER: IBM PC compatible
 i OPERATING SYSTEM: PC-DOS/MS-DOS
 i SOFTWARE: PatentIn Release #1.0, Version #1.30
 i CURRENT APPLICATION DATA:
 i APPLICATION NUMBER: US/09/030,606
 i FILING DATE: 25-FEB-1998
 i CLASSIFICATION:
 i ATTORNEY/AGENT INFORMATION:
 i NAME: Maki, David J.
 i REGISTRATION NUMBER: 31,392
 i REFERENCE/DOCKET NUMBER: 210121-428C3
 i TELECOMMUNICATION INFORMATION:
 i TELEPHONE: (206) 622-4900
 i TELEFAX: (206) 682-6031
 i INFORMATION FOR SEQ ID NO: 114:
 i SEQUENCE CHARACTERISTICS:

| Copyright (c) 1993 - 2005 Compugen Ltd. | GenCore version 5.1.6 | ubiquitin-specific protease | | | |
|--|---|--------------------------------|--------|----------|--|
| OM protein - protein search, using bw model | | hypothetical protein - | | | |
| Run on: | February 5, 2005, 19:49:45 ; Search time 18.678 Seconds (without alignments) | MEGFI protein - | | | |
| Title: | US-09-780-669-114_COPY_151_169 | Glucosyltransferase | | | |
| Perfect score: | 106 | hypothetical protein | | | |
| Sequence: | 1 GFTNYTDFDSFYKNSA 19 | FMN-containing NAD | | | |
| Scoring table: | BLOSUM62 | tetraspan TSPAN-6 | | | |
| | Gapop 10.0 , Gapext 0.5 | hypothetical protein | | | |
| Searched: | 283416 seqs, 96216763 residues | protein F2D10.2 [i] | | | |
| Total number of hits satisfying chosen parameters: | 283416 | hypothetical protein | | | |
| Minimum DB seq length: 0 | | hypothetical protein | | | |
| Maximum DB seq length: 2000000000 | | hypothetical protein | | | |
| Post-processing: Minimum Match 0% | | alpha-glucosidase | | | |
| Maximum Match 100% | | probable arsenical | | | |
| Listing First 45 summaries | | conserved hypothetical protein | | | |
| Database : | PIR_79:* | aldehyde 1-dimerase | | | |
| | 1: Pirl1:* | SOX6 protein - mou | | | |
| | 2: Pir2:* | | | | |
| | 3: Pir3:* | | | | |
| | 4: pir4: * | | | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | |
| | | SUMMARIES | | | |
| Result No. | Score | Query Match | Length | DB ID | Description |
| 1 | 106 | 100.0 | 241 | 2 A59262 | tetraspan TSPAN-1 T-cell acute lymph tetrspan TSPAN-3 protein CL3B9_4 [i] |
| 2 | 51 | 48.1 | 244 | 1 A59268 | hypothetical protein |
| 3 | 49 | 46.2 | 253 | 2 A59264 | ABC transporter (P |
| 4 | 46.5 | 43.9 | 644 | 2 E88487 | X-pro dipeptidyl-P x-pro dipeptidyl-P |
| 5 | 46 | 43.4 | 379 | 1 RGKLA | GTP-binding regula |
| 6 | 45 | 42.5 | 308 | 2 AE2960 | hypothetical protein |
| 7 | 45 | 42.5 | 319 | 2 A98323 | ABC transporter |
| 8 | 45 | 42.5 | 322 | 2 B2078 | T-cell acute lymphoblastic leukemia associated antigen 1 - human |
| 9 | 45 | 42.5 | 401 | 2 H97714 | N;Alternate names: cell surface glycoprotein (clone A15); TALLA-1 |
| 10 | 45 | 42.5 | 431 | 2 T38260 | C;Species: Homo sapiens (man) |
| 11 | 45 | 42.5 | 648 | 2 B84139 | C;Date: 23-Feb-1996 #sequence_revision 23-Aug-1996 |
| 12 | 45 | 42.5 | 757 | 2 D95103 | C;Accession: I39368; I54784 |
| 13 | 45 | 42.5 | 795 | 2 B97971 | R;Enni, N.; Kitaori, K.; Seto, M.; Ueda, R.; Saito, H.; Takahashi, T. |
| 14 | 45 | 42.5 | 1451 | 2 I40325 | Immunogenetics 37, 193-198, 1993 |
| 15 | 44.5 | 42.0 | 459 | 2 AD1787 | A;Title: Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superficial |
| 16 | 44 | 41.5 | 203 | 2 D84221 | A;Reference number: I39368; MUID:93131291; PMID:8420826 |
| 17 | 44 | 41.5 | 384 | 2 T44652 | A;Accession: I39368 |
| 18 | 44 | 41.5 | 1069 | 2 C85349 | A;Molecule type: mRNA |
| 19 | 44 | 41.5 | 1093 | 2 T08551 | A;Cross-references: 1-244 <RES> |
| 20 | 43.5 | 41.0 | 1941 | 2 T23979 | A;Experimental source: immature T cell line HPB-ALL |
| 21 | 43.5 | 41.0 | 1943 | 2 T23986 | R;Fukagi, S.; Fujikawa, K.; Imai, T.; Fukuhara, N.; Fukudome, K.; Minegishi, M.; Tsuchiy |
| 22 | 43 | 40.6 | 98 | 2 S26932 | Int. J. Cancer 61, 706-715, 1995 |
| 23 | 43 | 40.6 | 238 | 1 I38016 | C;Title: Identification of a highly specific surface marker of T-cell acute lymphoblasti |
| 24 | 43 | 40.6 | 245 | 2 A59258 | A;Reference number: I54784; MUID:95288314; PMID:7768645 |
| 25 | 43 | 40.6 | 552 | 2 T27424 | A;Accession: I54784; |
| 26 | 43 | 40.6 | 684 | 2 T37944 | A;Status: translated from GB/EMBL/DDJB |
| 27 | 43 | 40.6 | 729 | 2 F83725 | A;Molecule type: mRNA |
| 28 | 43 | 40.6 | 773 | 2 A71079 | A;Residues: 1-244 <RE2> |
| 29 | 43 | 40.6 | 773 | 2 D75033 | |

A;Cross-references: GB:D29808; NID:9475005; PIDN:BAA06191.1; PID:9475006
 C;Genetics:
 A;Gene: GDB:MKS1; DKS1692E; A15; TALLA-1
 A;Cross-references: GDB:202921
 A;Map position: Xg11-Xg11
 C;Superfamily: CD9 antigen
 C;Keywords: glycoprotein; surface antigen; transmembrane protein
 F;1-11/Domain: intracellular #status predicted <CY1>
 F;12-35/Domain: transmembrane #status predicted <TM1>
 F;36-51/Domain: extracellular #status predicted <EX1>
 F;52-76/Domain: transmembrane #status predicted <TM2>
 F;77-80/Domain: intracellular #status predicted <CY2>
 F;81-102/Domain: extracellular #status predicted <TM3>
 F;103-202/Domain: transmembrane #status predicted <EX2>
 F;208-232/Domain: transmembrane #status predicted <TM4>
 F;233-244/Domain: intracellular #status predicted <CY3>
 F;49,150-172,183/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 48.1%; Score 51; DB 1; Length 244;
 Best Local Similarity 52.9%; Pred. No. 1.7%; Indels 0; Gaps 0;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 GFNNYTDPEPSPKEN 17
 Db 147 GVQNYTNWNTSPYPLEH 163

RESULT 3
 A59264
 tetraspan - human
 tetraspan-3 - human
 C;Species: Homo sapiens (man)
 C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
 C;Accession: A59264
 R;Todd, S.C.; Doctor, V.S.; Levy, S.
 Biochim. Biophys. Acta 1399, 101-104, 1998
 A;Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.
 A;Reference number: A59258; PMID:98390578; PMID:9714163
 A;Accession: A59264
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-253 <TOD>
 A;Cross-references: UNIPROT:060637; GB:AF054840; NID:92997744; PIDN: AAC69716.1; PID:92997744; PIDN: AAC69716.1; PID:92997744
 C;Genetics:
 A;Gene: TSPAN-3
 C;Superfamily: CD9 antigen

Query Match 46.2%; Score 49; DB 2; Length 253;
 Best Local Similarity 50.0%; Pred. No. 3.7%; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GFNNYTDPEPSPKEN 16
 Db 149 GHNNYSDWENTDWFK 164

RESULT 4
 E88487
 protein C13B9.4 [imported] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C;Accession: E88487
 R;anonymous. The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes, development, behavior, and death
 A;Reference number: A50000; MURD:99065613; PMID:9851916
 A;Note: see websites geno.sanger.ac.uk/Projects/C_elegans/ and www.sanger.ac.uk/gsc/C_elegans/
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
 A;Accession: E88487
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-644 <STO>
 A;Cross-references: UNIPROT:Q09460; GB:chr_III; PIDN: AAA62517.1; PID:9687811; GSPDB:GN00
 C;Genetics:

A;Gene: C13B9.4
 A;Map position: 3
 Query Match 43.9%; Score 46.5%; DB 2; Length 644;
 Best Local Similarity 47.4%; Pred. No. 26; Mismatches 4; Indels 5; Gaps 1;
 Matches 9; Conservative 9; Mismatches 1; Indels 6; Gaps 5;
 Qy 1 GFNNYTDPEPSPKEN 14
 Db 132 GWTINPTVCFKIDYEAKYF 150

RESULT 5
 RGXLA
 GTP-binding regulatory protein Gs alpha chain (adenylate cyclase-stimulating) - African clawed frog
 N;Alternate names: guanine nucleotide binding protein Gs alpha chain; heterotrimeric G-protein
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C;Accession: S11047
 R;Olale, J.; Martinez, S.; Purcell, P.; Jorquera, H.; Codina, J.; Birnbaumer, L.; Allende, FEBs Lett. 268, 27-31, 1990
 A;Title: Molecular cloning and sequence determination of four different cDNA species coding for the Gs alpha chain
 A;Reference number: S11045; MUID:90346157; PMID:2116977
 A;Accession: S11047
 A;Molecule type: mRNA
 A;Residues: 1-79 <COLA>
 A;Cross-references: UNIPROT:P24799; GB:X556091; NID:964713; PIDN:CAA39571.1; PID:964714
 C;Comment: The G proteins are a family of quanine nucleotide-binding proteins that relay signals. The beta and gamma chains, required for GTPase activity, appear to be common to all G-proteins. The alpha chain is specific for each type of G protein.
 C;Superfamily: GTP-binding regulatory protein Gs alpha chain
 C;Keywords: alternative splicing; blocked amino end; GTP binding; heterotrimer; lipoprotein P; 2-3'Product: GTP-binding regulatory protein Gs alpha chain #status predicted <NAT>
 P;47-54/Region: nucleotide-binding motif A (P-loop)
 P;2-37/Region: nucleotide-binding motif B (NXXD)
 P;27-28/Region: GTP-binding NXXD motif
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;3/Binding site: palmitate (Cys) (covalent) #status predicted
 F;186/Modified site: ADP-ribooylarginine (Arg) (by cholera toxin) #status predicted
 Query Match 43.4%; Score 46; DB 1; Length 379;
 Best Local Similarity 60.0%; Pred. No. 17%; Indels 0; Mismatches 4; Gaps 0;
 Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 NYTFDDEPSPKEN 18
 Db 121 NYKDFEFSPEFYHT 135

RESULT 6
 AB2960
 hypothetical protein malp [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AB2960
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, Y.; Woo, L.; Erage, G.; Gillet, W.; Grant, C.; Ghentner, D.; Kutyavina, T.; Levy, R.; Li, M.; McClellan, P.; Karp, P.; Romero, P.; Zhang, S.
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Perry, M.; Gordon-Kamm, F.; Ester, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AE2960
 A;Molecule type: DNA
 A;Residues: 1-308 <KUR>
 A;Cross-references: UNIPROT:Q8UT4; GB:AE008689; PIDN: AAL4099.1; PID:917741667; GSPDB:GN
 C;Genetics:
 A;Gene: malp
 A;Map position: linear chromosome ugpa
 C;Superfamily: inner membrane protein ugpa

Query Match 42.5%; Score 45; DB 2; Length 308;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;
C;Species: Rickettsia conorii C;Sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97714
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A;Reference number: A97700; PMID:21442074; PMID:11557833
A;Accession: H97714
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <KUR>
A;Cross-references: UNIPROT:Q92JE7; GB:AE006914; PIDN:AAL02658.1; PIDN:AA006914; PIDN:915619162; GSPDB:G
C;Genetics:
C;Superfamily: aspartate transaminase
C;Keywords: aminotransferase
C;Gene: actA
C;Protein:
C;Genetics:
C;Superfamily: aspartate transaminase
C;Keywords: aminotransferase
C;Gene: actA
A;Accession: A98323
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2223-2228, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58 [strain: ATCC 11743; M59; MTED:21608551; PMID:11743194
A;Accession: A98323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <KUR>
A;Cross-references: UNIPROT:Q8UAT4; GB:AE007870; PIDN:AAK90107.1; PIDN:g15160096; GSPDB:G
C;Genetics:
A;Gene: AGR_L_3068
A;Map Position: linear chromosome 0
C;Superfamily: inner membrane protein ugPA
Query Match 42.5%; Score 45; DB 2; Length 319;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
C;Species: Schizosaccharomyces pombe C;Sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38260
R;Harris, D.; Squares, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Accession: T38260
A;Reference number: Z21782
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-431 <SHAR>
A;Cross-references: UNIPROT:Z99753; ENBLCAB16876.1; GSPDB:GN000666; SPDB:SP
C;Genetics:
C;Superfamily: strain 972h-; cosmid C23C4
C;Keywords:
C;Gene: SPAC23C4.05C
A;Map position: 1
A;Introns: 23/1
Query Match 42.5%; Score 45; DB 2; Length 431;
Best Local Similarity 51.1%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
C;Species: Schizosaccharomyces pombe C;Sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: B84139
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; PMID:11759585; PMID:11759440
A;Accession: AB2078
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-322 <KUR>
A;Cross-references: UNIPROT:Q8YV05; GB:BA000019; PIDN:BAB73875.1; PIDN:g17131267; GSPDB:G
A;Experimental source: strain PC C 7120
C;Genetics:
A;Gene: alr2176
C;Superfamily: ferrichrome-iron transport protein fecB
Query Match 42.5%; Score 45; DB 2; Length 322;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
C;Species: Bacillus halodurans C;Sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: B84139
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its resistance to organic solvents
A;Reference number: A83650; PMID:20512582; PMID:11050132
A;Accession: B84139
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-648 <STO>
A;Cross-references: UNIPROT:Q9K618; GB:AP001520; PIDN:BA000004; PIDN:910176401; PIDN:BAB076
C;Genetics:
A;Experimental source: strain C-125
A;Gene: BH3914
RESULT 9
H97714
aspartate transaminase (EC 2.6.1.1) - *Rickettsia conorii* (strain Malish 7)

RESULT 14
 Query Match Score 45; DB 2; Length 648;
 Best Local Similarity 72.4%; Pred. No. 44;
 Matches 1; Mismatches 2; Indels 0; Gaps 0;
 C:Species: Streptococcus pneumoniae
 C:Accession: D95103
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Hickney, E.K.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,
 Science 293, 498-506, 2001.
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
 A;Reference number: A92000; PMID:21357209; PMID:11463916
 A;Accession: D95103
 A;Status: Preliminary
 A;Residues: 1-757 <KUR>
 A;Cross-references: UNIPROT:Q97RQB; GB:AE005672; PIDN:AAK75021.1; PID:914972369; GSPPDB:C
 C;Experimental source: strain TIGR4
 A;Gene: SP0894
 C;Superfamily: Lactococcus X-Pro dipeptidyl-peptidase

Query Match Score 45; DB 2; Length 757;
 Best Local Similarity 44.4%; Pred. No. 53;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 C:Species: Streptococcus pneumoniae (EC 3.4.14.11) [Imported] - *Streptococcus pneumoniae* (strain
 B97971)
 C:Accession: B97971
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 R;Hoskins, J.A.; Alborn, Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
 leBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 Y.; Sun, P.M.; Winkler, M.E.
 J.; Bacteriol. 183, 5709-5717, 2001.
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A;Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
 A;Reference number: A97672; PMID:21429245; PMID:11544234
 A;Accession: B97971
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q8DQB7; GB:AE007317; PIDN:AAK99598.1; PID:915458392; GSPPDB:C
 C;Genetics:

Query Match Score 45; DB 2; Length 795;
 Best Local Similarity 44.4%; Pred. No. 56;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

RESULT 15
 Query Match Score 45; DB 2; Length 1451;
 Best Local Similarity 57.1%; Pred. No. 1-1e-02;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 C:Species: Listeria innocua (strain Clip11262)
 C:Accession: AD1787
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 28-Jul-2003
 R;Glasier, P.; Frangoul, L.; Buchrisser, C.; Amend, A.; Baquero, F.; Berche, P.; Blooecker,
 J.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, H.,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001.
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Mat
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,
 A;Reference number: AB1077; PMID:21537219; PMID:11679669
 A;Accession: AD1787
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-459 <GLA>
 A;Cross-references: GB:AL592022; PIDN:CAC98068.1; PID:916415377; GSPPDB:GN00178
 A;Experimental source: strain Clip11262
 C;Genetics:
 C:Superfamily: lysine decarboxylase
 A;Reference number: AB1077; PMID:21537219; PMID:11679669
 A;Accession: AD1787
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-459 <GLA>
 A;Cross-references: GB:AL592022; PIDN:CAC98068.1; PID:916415377; GSPPDB:GN00178
 A;Experimental source: strain Clip11262
 C;Genetics:
 C:Superfamily: lysine decarboxylase
 A;Reference number: AB1077; PMID:21537219; PMID:11679669
 A;Accession: AD1787
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-195 <KUR>
 A;Cross-references: UNIPROT:Q8DQB7; GB:AE007317; PIDN:AAK99598.1; PID:915458392; GSPPDB:C
 C;Genetics:

Query Match Score 45; DB 2; Length 795;
 Best Local Similarity 44.4%; Pred. No. 56;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Search completed: February 5, 2005, 20:05:44
 Job time : 20.678 secs

| Scoring table: | BLOSUM62 | | | | | | |
|--|--|-----------|-----------|-----------|--------------|-----------|-------------------------|
| Searched: | 1612378 seqs, 512079187 residues | | | | | | |
| Total number of hits satisfying chosen parameters: | 1612378 | | | | | | |
| Minimum DB seq length: | 0 | | | | | | |
| Maximum DB seq length: | 200000000 | | | | | | |
| Post-processing: | Minimum Match 0% Maximum Match 100% Listing first 45 summaries | | | | | | |
| Database : | UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: * | | | | | | |
| Pred. | No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | |
| SUMMARIES | | | | | | | |
| Result No. | Query | Score | Match | Length | DB | ID | Description |
| - - - - - | - - - - - | - - - - - | - - - - - | - - - - - | - - - - - | - - - - - | - - - - - |
| 1 | 106 | 100.0 | 241 | 1 | TSN1_HUMAN | 060335 | homo sapien |
| 2 | 62 | 58.5 | 241 | 2 | QAYR9 | 06ayr9 | rattus norvegicus |
| 3 | 60 | 56.6 | 240 | 2 | Q9UJ59 | 099j59 | mus musculus |
| 4 | 56 | 52.8 | 248 | 2 | Q81OP9 | 081op9 | mus musculus |
| 5 | 52 | 49.1 | 96 | 2 | Q7VAG9 | 07vg99 | prochlorococcus marinus |
| 6 | 51 | 48.1 | 52 | 2 | Q72Z15 | 07z15 | homo sapien |
| 7 | 51 | 48.1 | 52 | 2 | Q7YQH1 | 07yqh1 | pan troglodytes |
| 8 | 51 | 48.1 | 52 | 2 | Q7YQH2 | 07yqh2 | pan troglodytes |
| 9 | 51 | 48.1 | 240 | 2 | Q6GP11 | 06gp11 | xenopus laevis |
| 10 | 51 | 48.1 | 244 | 1 | T4S2_PANTHER | 07yq10 | pan troglodytes |
| 11 | 51 | 48.1 | 244 | 1 | T4S2_PONPY | 07yq19 | pongo pygmaeus |
| 12 | 51 | 48.1 | 244 | 2 | Q72Z26 | 07z26 | homo sapien |
| 13 | 51 | 48.1 | 249 | 1 | T4S2_HUMAN | 041732 | homo sapien |
| 14 | 50 | 47.2 | 433 | 2 | Q89XR2 | 089xr2 | bradyrhizobium elkanii |
| 15 | 50 | 47.2 | 434 | 2 | Q6N118 | 06n118 | rhodopseudomonas |
| 16 | 50 | 47.2 | 728 | 2 | Q9UNW8 | 09unw8 | sulfobacillus |
| 17 | 49 | 46.2 | 157 | 2 | Q8R0Q6 | 08r0q6 | mus musculus |
| 18 | 49 | 46.2 | 235 | 2 | Q7RD42 | 07rd42 | plasmocitomyces |
| 19 | 49 | 46.2 | 240 | 2 | Q6P420 | 06p420 | xenopus laevis |
| 20 | 49 | 46.2 | 244 | 2 | Q6PDN6 | 06pdn6 | mus musculus |
| 21 | 49 | 46.2 | 244 | 2 | Q6DDY1 | 06ddy1 | xenopus laevis |
| 22 | 49 | 46.2 | 245 | 2 | Q8BPU2 | 08bpu2 | mus musculus |
| 23 | 49 | 46.2 | 249 | 1 | T4S2_MOUSE | 06283 | mus musculus |
| 24 | 49 | 46.2 | 253 | 1 | T4S8_HUMAN | 060337 | homo sapien |
| 25 | 49 | 46.2 | 253 | 2 | T4S8_MOUSE | 06qrs3 | mus musculus |
| 26 | 49 | 46.2 | 254 | 2 | Q66H06 | 066h06 | rattus norvegicus |
| 27 | 49 | 46.2 | 254 | 2 | Q8ILA9 | 08ila9 | plasmocitomyces |
| 28 | 49 | 46.2 | 424 | 2 | Q89GR4 | 089gr4 | bradyrhizobium elkanii |
| 29 | 48 | 45.8 | 234 | 2 | Q7T2B8 | 07t2b8 | brachydanio rerio |
| 30 | 48 | 45.3 | 157 | 2 | Q9GMU7 | 09gmu7 | macaca fasciata |
| 31 | 48 | 45.3 | 506 | 2 | Q8XJJ0 | 08xjj0 | oryza sativa |

ALIGNMENTS

| | | | | |
|------------|--|----------|------|---------|
| RESULT 1 | TSN1_HUMAN | STANDARD | PRT; | 241 AA. |
| ID | 060335; 060745; | | | |
| AC | 060745; | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | |
| DE | Tetraspanin 1 (Tspan-1) (Tetraspan NET-1) (Tetraspanin TM4-C). | | | |
| GN | Name=TSPAN1; | | | |
| OS | Homo sapiens (Human) | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| NCBI_TaxID | 9606; | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=9839078; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6; | | | |
| RA | Todd S.C., Doctor V.S., Levy S.; | | | |
| RT | "Sequences and expression of six new members of the tetraspanin/TM4SF family.", | | | |
| RL | Biochim. Biophys. Acta 1399:101-104 (1998). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Rubinstein E., Serru V., Boucheix C.; | | | |
| RL | "New tetraspans identified in the EST database", Submitted (MAY-1998) to the EMBL/GenBank/DBJ database. | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Puls K.L., Ni J., Liu D., Morahan G., Wright M.D.; | | | |
| RA | "The molecular characterization of four tetraspansin.", Submitted (MAY-1999) to the EMBL/GenBank/DBJ database. | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Colon; | | | |
| RX | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuller G.D., Altschul S.P., Zeeberg B.R., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bobek S.A., McEwan P.J., McKernan K.J., Malek J.A., Garcia A.M., Hale S., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Helton B., Ketteman M., Madan A., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickeson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Scherich A., Schein J.E., Jones S.J.M., Marrs M.A.; | | | |
| RA | "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). | | | |

-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

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CC AF054338; AAC69714.;
 EMBL; AF05398; AAC17119.;
 EMBL; AF133425; AAF08364.;
 EMBL; BC013404; AAH13404.;
 PIR; A5262; A59242.
 H-invDB: HIX0000543;
 DR / GO: 0016021; C:integral to membrane; TAS.
 InterPro: IPRO000301; Transmem 4.
 DR IPRO008932; Tetraspanin.
 DR PF00335; Tetraspanin; I.
 DR PR00559; TMFOUR.
 DR PRINTS; PS00421; TM4_1; FALSE_NEG.
 KW Glycoprotein; Transmembrane.
 DOMAIN 1 11 Cytoplasmic (Potential).
 FT DOMAIN 12 32 Potential; TMFOUR.
 FT DOMAIN 33 52 Extracellular (Potential).
 FT TRANSMEM 53 73 Potential.
 FT DOMAIN 74 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 109 Potential.
 FT DOMAIN 110 211 Extracellular (Potential).
 FT TRANSMEM 212 232 Potential.
 FT DOMAIN 233 241 Cytoplasmic (Potential).
 FT CARBOHYD 141 141 N-linked (GlcNAc .) (Potential).
 FT CARBOHYD 154 154 N-linked (GlcNAc .) (Potential).
 FT CARBOHYD 178 178 N-linked (GlcNAc .) (Potential).
 FT CARBOHYD 184 184 N-linked (GlcNAc .) (Potential).
 FT CONFLICT 189 189 K -> E (in Ref. 1)
 SQ SEQUENCE 241 AA; 26301 MN; A938AB07147CB884 CRC64;

Query Match 100.0%; Score 106; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFNNYTDFFDSFYKFN 19
 Db 151 GFNNYTDFFDSFYKFN 169

RESULT 2
 Q6AYR9 PRELIMINARY; PRT; 241 AA.
 AC Q6AYR9; PRELIMINARY; PRT; 241 AA.
 AC Q6AYR9; PRELIMINARY; PRT; 241 AA.
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Tetraspan 1.
 GN Name=NCGB3753;
 OS Rattus norvegicus (Rat).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Rodentia; Muridae; Murinae; Rattus.
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN SEQUENCE FROM N.A.
 RC STRAIN=NMR1; TISSUE=Mammary tumor;
 RC MEILINE=2238825; PubMedID=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Mullahy S.J.,
 RA Klausner R.D., Collins F.S., Wagner L., Schuler G.D., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buerow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkins R.F., Jordan R., Rubin G.M., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rabah S.S., Loqueilano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bokay S.A., McEwan P.J., McKernan K.J., Malek J.A., Grouse L.H., Derge J.G.,
 RA Richards S., Worley K.C., Grupe L.H., Schuler G.D., Schaefer C.F., Bhat N.K.,
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Mullahy S.J.,
 RA Altschul S.F., Zeeberg B., Buerow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Blakesley R.W., Buetow K.H., Wagner L., Schaefer C.F., Bhat N.K.,
 RA Whiting M., Madan A., Ketteman M., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schaefer C.F.,
 RA Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RT [2].
 RN SEQUENCE FROM N.A.
 RC TISSUE=Kidney,
 RA Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: BC07893; AAH17938; 1; -.
 GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR002229; RhesusRHD.
 DR InterPro; IPR008952; Tetraspanin.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; Tetraspanin; I.
 DR PRINTS; PR00254; RhesusRHD.
 DR PROSITE; PS00421; TMFOUR.
 DR PROSITE; PS00421; TM4_1.; 1.
 DR SEQUENCE 241 AA; 26301 MN; 9118E865464D1A70 CRC64;
 DR SEQUENCE 241 AA; 26301 MN; 9118E865464D1A70 CRC64;

B'g. 5 EYONYTNWSTSBYFI.EH 21

or send an email to license@isb-sib.ch).

| | | | | |
|--|-----------------------|--------------------------|--------------------------------------|--------------------------------------|
| CC | FT DOMAIN | 71 | 81 | Cytoplasmic (Potential). |
| CC | FT TRANSMEM | 82 | 107 | Extracellular (Potential). |
| DR | FT DOMAIN | 108 | 208 | Potential. |
| DR | FT TRANSMEM | 209 | 229 | Cytoplasmic (Potential). |
| DR | FT DOMAIN | 230 | 244 | N-linked (GlcNAc . . .) (Potential). |
| DR | FT CARBOHYD | 49 | 49 | N-linked (GlcNAc . . .) (Potential). |
| DR | FT CARBOHYD | 150 | 150 | N-linked (GlcNAc . . .) (Potential). |
| DR | FT CARBOHYD | 153 | 153 | N-linked (GlcNAc . . .) (Potential). |
| DR | FT CARBOHYD | 172 | 172 | N-linked (GlcNAc . . .) (Potential). |
| DR | FT CARBOHYD | 183 | 183 | N-linked (GlcNAc . . .) (Potential). |
| DR | FT TRANSMEM | 35 | 35 | Cytoplasmic (Potential). |
| FT DOMAIN | 36 | 51 | Extracellular (Potential). | |
| FT TRANSMEM | 52 | 70 | Potential. | |
| FT DOMAIN | 71 | 81 | Cytoplasmic (Potential). | |
| FT TRANSMEM | 82 | 107 | Extracellular (Potential). | |
| FT DOMAIN | 108 | 208 | Potential. | |
| FT TRANSMEM | 209 | 229 | Cytoplasmic (Potential). | |
| FT DOMAIN | 230 | 244 | N-linked (GlcNAc . . .) (Potential). | |
| FT CARBOHYD | 49 | 49 | N-linked (GlcNAc . . .) (Potential). | |
| FT CARBOHYD | 150 | 150 | N-linked (GlcNAc . . .) (Potential). | |
| FT CARBOHYD | 153 | 153 | N-linked (GlcNAc . . .) (Potential). | |
| FT CARBOHYD | 172 | 172 | N-linked (GlcNAc . . .) (Potential). | |
| FT CARBOHYD | 183 | 183 | N-linked (GlcNAc . . .) (Potential). | |
| SQ SEQUENCE | 244 AA; | 26945 MW; | 656EA94EE19050B CRC64; | |
| RESULT 12 | Query Match | 48.1% | Score 51; | DB 1; Length 244; |
| | Best Local Similarity | 52.9% | Pred. No. 8.5; | PRT; 244 AA. |
| | Matches | 9; | Conservative | 3; Mismatches |
| | Qy | 1 GFTNYTDFEDSPYFKEN 17 | | |
| | Db | 147 GVQNYTNWTSPPYLEH 163 | | |
| RESULT 13 | Query Match | 48.1% | Score 51; | DB 1; Length 244; |
| | Best Local Similarity | 52.9% | Pred. No. 8.5; | PRT; 244 AA. |
| | Matches | 9; | Conservative | 3; Mismatches |
| | Qy | 1 GFTNYTDFEDSPYFKEN 17 | | |
| | Db | 147 GVQNYTNWTSPPYLEH 163 | | |
| RESULT 11 | Query Match | 48.1% | Score 51; | DB 1; Length 244; |
| | Best Local Similarity | 52.9% | Pred. No. 8.5; | PRT; 244 AA. |
| | Matches | 9; | Conservative | 3; Mismatches |
| | Qy | 1 GFTNYTDFEDSPYFKEN 17 | | |
| | Db | 147 GVQNYTNWTSPPYLEH 163 | | |
| T4S2_PONPY | STANDARD; | PRT; | 244 AA. | |
| ID T4S2_PONPY | | | | |
| AC QYIQK5; | | | | |
| DT 05-JUL-2004 (Rel. 44, Created) | | | | |
| DT 05-JUL-2004 (Rel. 44, Last sequence update) | | | | |
| DT 05-JUL-2004 (Rel. 44, Last annotation update) | | | | |
| DE Transmembrane 4 superfamily member 2. | | | | |
| GN Name=TM4SF2; | | | | |
| OS Pongo pygmaeus (Orangutan). | | | | |
| OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; | | | | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| NCBI_TaxID=9600; | | | | |
| RN [1] | | | | |
| RP SEQUENCE FROM N.A. | | | | |
| RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134; | | | | |
| RA Kitano T., Schwarz C., Nickel B., Paabo S.; | | | | |
| RT "Gene diversity patterns at 10 X-chromosomal loci in humans and chimpanzees"; | | | | |
| RT Mol. Biol. Evol. 20:1281-1289(2003). | | | | |
| RT EMBL; AB102665; BAC81134 1; -. | | | | |
| RT GO; GO:0016021; C:integral to membrane; IEA. | | | | |
| DR InterPro; IPR008552; Tetraspanin. | | | | |
| DR InterPro; IPR003031; Transmem 4. | | | | |
| DR Pfam; PF00335; Tetraspanin; T. | | | | |
| KW Transmembrane. | | | | |
| PROSITE; PS00421; TM4_1; UNKNOWN_1. | | | | |
| KW SEQUENCE | 244 AA; | 26972 MW; | 53B003EB5A8A202C CRC64; | |
| RESULT 13 | Query Match | 48.1% | Score 51; | DB 2; Length 244; |
| | Best Local Similarity | 52.9% | Pred. No. 8.5; | PRT; 244 AA. |
| | Matches | 9; | Conservative | 3; Mismatches |
| | Qy | 1 GFTNYTDFEDSPYFKEN 17 | | |
| | Db | 147 GVQNYTNWTSPPYLEH 163 | | |
| T4S2_HUMAN | STANDARD; | PRT; | 249 AA. | |
| ID T4S2_HUMAN | | | | |
| AC Q9UEY9; | | | | |
| DT 01-NOV-1995 (Rel. 32, Created) | | | | |
| DT 28-FEB-2003 (Rel. 41, Last sequence update) | | | | |
| DT 05-JUL-2004 (Rel. 44, Last annotation update) | | | | |
| DE Transmembrane 4 superfamily member 2 (Cell surface glycoprotein A15); | | | | |
| DE (T-acute lymphoblastic leukemia associated antigen 1) (TALLA-1) | | | | |
| DE (Membrane component, X chromosome, surface marker 1) (CD231 antigen). | | | | |
| GN Name=TM4SF2; Synonyms Human. | | | | |
| OS Homo sapiens (Human). | | | | |
| OC EuKaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; | | | | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX NCBI_TaxID=9600; | | | | |

SEQUENCE FROM N.A.
STRAIN=USDA110;
RC MEDLINE=224498; PubMed=12597275;
RX Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idezawa K., Iriuchi M., Kawashima K.,
RA Kohara M., Matsunoto M., Shimpo S., Tsurioka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res 9:189-197 (2002).
DR EMBL; AP005935; BAC45510.1; -.
DR HSSP; P1GCO; 1GCO;
DR GO; GO:0016839; P: lyase activity; IEA.
DR GO; GO:0016765; P: transferase activity, transferring alkyl or . . . ; IEA.
DR GO; GO:0006520; P: amino acid metabolism; IEA.
DR InterPro; IPR000277; Cys_Met_Meta_PP.
DR InterPro; IPR006235; OAH_OAS_Sulphy.
DR Pfam; PF01053; Cys_Met_Meta_PP; 1.
DR TIGRFAMs; TIGR01326; OAH_OAS_Sulphy; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 433 AA; 46823 MW; 5A4110C4615F70BS CRC64;

Query Match 47.2%; Score 50; DB 2; Length 433;
Best Local Similarity 61.5%; Pred. No. 24; Gaps 0;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 FTNYTDFPSPYF 14
:||| | |||:
Db 313 WVNXTGFPPSPYY 325

RESULT 15
Q6N118 PRELIMINARY; PRT; 434 AA.
ID Q6N118; AC Q6N118; PRELIMINARY; PRT; 434 AA.
DT 05-JUL-2004 (TREMBrel. 27, Created)
DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)
DE Hemocysteine synthase (EC 2.5.1.49).
Name=methyl; OrderedLocusName=RPAA591;
GN OS Rhodopseudomonas palustris.
RA Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Peplow D.J., Lang B.J.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Perez C.,
RA Harrison P.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61 (2004).
DR GO; GO:0003961; FO-O-acetylhomoserine aminocarboxyprolyltransf. . . ; IEA.
DR GO; GO:0006520; P: amino acid metabolism; IEA.
DR InterPro; IPR000277; Cys_Met_Meta_PP.
DR InterPro; IPR006235; OAH_OAS_Sulphy.
DR Pfam; PF01053; Cys_Met_Meta_PP; 1.
DR TIGRFAMs; TIGR01326; OAH_OAS_Sulphy; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 434 AA; 46947 MW; B7846EA96BA911FC CRC64;
Query Match 47.2%; Score 50; DB 2; Length 434;
Best Local Similarity 61.5%; Pred. No. 24; Gaps 0;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 FTNYTDFPSPYF 14
:||| | |||:
Db 313 WVNXTGFPPSPYY 325

ALIGNMENTS

```

database : A_Genesseq_16Dec04;*
Accession : AAM01158;
Description : Human prostate-specific peptide used in epitope mapping studies #15.
Organism : Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis.
Sequence :
XX
AC
XX
XX
DT
XX
DE
XX
KW
KW
KW
XX

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of random score distribution.

| | | |
|--------------|----|-----------------|
| Pred. No. | OS | XX |
| Homosapiens. | PN | W0200151633-A2. |

SUMMARIES
PD 19-JUL-2001.
XX
PP 16-JAN-2001; 2001WO-US001574.
PR

| NO. | Score | Match Length | DB | ID | Description | PR |
|-----|-------|--------------|-----|----|--|----------------------|
| 1 | 116 | 100.0 | 20 | 4 | AAM01158 Human pro AAU63803 Human pro AAG93043 Human pro ABU1694 Prostate ABB95263 Epitope in Abra4375 Prostate | XX |
| 2 | 116 | 100.0 | 20 | 4 | AAM01158 Human pro AAU63803 Human pro AAG93043 Human pro ABU1694 Prostate | PA |
| 3 | 116 | 100.0 | 20 | 4 | AAG93043 Human pro ABU1694 Prostate | XX |
| 4 | 116 | 100.0 | 20 | 4 | ABU1694 Prostate | PI |
| 5 | 116 | 100.0 | 20 | 5 | ABB95263 Epitope in Abra4375 Prostate | PI |
| 6 | 116 | 100.0 | 20 | 6 | ABR54375 | WPI; 2001-425873/45. |
| 7 | 116 | 100.0 | 20 | 7 | ADB13955 Human pro | DR |
| 8 | 116 | 100.0 | 20 | 7 | ADG26371 Human pro | XX |
| 9 | 116 | 100.0 | 172 | 7 | ADD6590 Human pro | PT |
| 10 | 116 | 100.0 | 174 | 8 | ADP81123 Protein o | PT |
| 11 | 116 | 100.0 | 214 | 8 | ADR65994 Human pro | PT |

Claim 2: Page 399; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytotoxic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. (I) can indicate the live of metastasis as well as the progression of cancer.

volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention

| | | |
|---|---|--|
| XX | CC | antigenic epitopes or domains of prostate specific proteins |
| Sequence 20 AA; | XX | Sequence 20 AA; |
| Query Match 100.0%; Score 116; DB 4; Length 20; | XX | Score 116; DB 4; Length 20; |
| Best Local Similarity 100.0%; Pred. No. 3.9e-10; | XX | Best Local Similarity 100.0%; Pred. No. 3.9e-10; |
| Matches 20; Conservative 0; Mismatches 0; | XX | Matches 20; Conservative 0; Mismatches 0; |
| Qy 1 KENSAFPFPPCCNDNVNTAN 20 | Qy | 1 KENSAFPFPPCCNDNVNTAN 20 |
| Db 1 KENSAFPFPPCCNDNVNTAN 20 | Db | 1 KENSAFPFPPCCNDNVNTAN 20 |
| RESULT 3 | | |
| AAG93043 | | |
| ID AAG93043 standard; peptide; 20 AA. | | |
| XX | XX | |
| AC AAG93043; | AC | |
| XX | XX | |
| DT 25-SEP-2001 (first entry) | DT | |
| XX | XX | Human prostate specific epitope mapping peptide #15. |
| DE Human prostate peptide mapping peptide #2. | DE | |
| XX | XX | Human prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA. |
| KW KW | KW | |
| KW Human; prostate cancer; SS; cytostatic; immunostimulant; tumour; antigen; epitope. | KW | |
| KW KW | KW | |
| XX Homo sapiens. | OS Homo sapiens. | |
| XX XX | XX | |
| PN WO200117032-A2. | PN WO200134802-A2. | |
| XX | XX | |
| PD 04-OCT-2001. | PD 17-MAY-2001. | |
| XX | XX | |
| PP 2000WO-US031904. | PP 09-NOV-2000, | |
| XX | XX | |
| PP 2001WO-US009919. | PR 12-NOV-1999; | |
| XX | PR 18-NOV-1999; | |
| PR 27-MAR-2001; 20001WO-US009919. | PR 18-NOV-1999; | |
| XX | XX | |
| PR 27-MAR-2000; 200001US-00536857. | (CORI-) CORIXA CORP. | |
| PR 09-MAY-2000; 200001US-00536810. | Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG, | |
| PR 12-MAY-2000; 200001US-00536810. | Pi Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A; | |
| PR 13-JUN-2000; 200001US-00593793. | XX | |
| PR 27-JUN-2000; 200001US-00605783. | DR WPI; 2001-308785/32. | |
| PR 09-AUG-2000; 200001US-00636215. | XX | |
| PR 29-AUG-2000; 200001US-00651236. | Isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P744P, P712P, P775P and B303D are located in a Genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. | |
| PR 02-OCT-2000; 200001US-00657299. | CC | |
| PR 10-OCT-2000; 200001US-00688166. | CC | |
| PR 09-NOV-2000; 200001US-00709729. | CC | |
| XX | CC | |
| PA (CORI-) CORIXA CORP. | CC | The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P744P, P712P, P775P and B303D are located in a Genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. |
| XX | CC | Prostate specific antigen (PSA) P501S was located on chromosome 1. |
| PI 2001-639232/73. | CC | Proteins either represent polynucleotide sequences used in the exemplification of the present invention |
| PI 2001-639232/73. | CC | |
| PS Page 400; 579pp; English. | CC | |
| XX | CC | |
| The invention relates to isolated prostate-specific polynucleotides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer, especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific peptide of the invention. The peptides either represent | | |
| XX | CC | |
| PS Sequence 20 AA; | CC | |
| XX | CC | |
| Query Match 100.0%; Score 116; DB 4; Length 20; | CC | |
| Best Local Similarity 100.0%; Pred. No. 3.9e-10; | CC | |
| Matches 20; Conservative 0; Mismatches 0; | CC | |
| Qy 1 KENSAFPFPPCCNDNVNTAN 20 | Qy 1 KENSAFPFPPCCNDNVNTAN 20 | |
| Db 1 KENSAFPFPPCCNDNVNTAN 20 | Db 1 KENSAFPFPPCCNDNVNTAN 20 | |

PA (WANG A.) WANG A.
 PA (SKEI Y.) SKEI Y. A. W.
 PA (HEPL/) HEPPL/
 PA (HEND/) HENDERSON R. A.
 XX
 Xu J., Dillon DC., Mitcham JL., Harlocker SL., Jiang Y., Kalos MD.;
 PI Fanger GR., Retter MW., Stolk JA., Day CH., Vedvick TS., Carter D.;
 PI Li SX., Wang A., Skei YAW., Hepler WT., Henderson RA.;
 XX
 DR WPI; 2002-255649/3-0.
 XX
 PS New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer.
 XX
 Claim 2: SEQ ID NO 505; 87PP; English.
 XX
 The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a
 CC peptide described in the invention.
 XX
 Sequence 20 AA;
 Query Match 100.0%; Score 116; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.9e-10; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 Qy 1 KENSAFPFCCNDNTAN 20
 Db 1 KENSAFPFCCNDNTAN 20
 RESULT 6
 ABR34375 ID ABR34375 standard; protein; 20 AA.
 XX
 AC ABR34375;
 XX
 DT 28-AUG-2003 (first entry)
 XX
 DB Prostate tumour specific related peptide for epitope mapping SEQ ID 505.
 XX
 Cytostatic; gene therapy; prostate-specific protein; PSP; human;
 KW immune response; prostate cancer.
 XX
 Homo sapiens.
 OS
 PN WO200289747-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 09-MAY-2002; 2002WO-US014753.
 XX
 PR 09-MAY-2001; 2001US-0085291.
 PR 29-JUN-2001; 2001US-0089514.
 PR 10-DEC-2001; 2001US-00012896.
 XX
 (CORIXA CORP.
 PA Xu J., Dillon DC., Mitcham JL., Harlocker SL., Jiang Y., Henderson RA;
 PI Kalos MD., Fanger GR., Retter MW., Stolk JA., Day CH., Vedvick TS.,
 PI Carter D., Li SX., Wang A., Skei YAW., Hepler WT., Hural J.;
 PI Mcneil PD., Houghton RL., Vinals Y De BassolsC., Foy TM., Watanabe Y;
 PI Deng T.;
 XX
 WPI; 2003-167130/16.
 XX
 New prostate-specific Proteins and genes, useful in gene therapy,
 PT particularly for stimulating an immune response in a patient, or treating
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 PT in a patient.
 XX

PS Example 18; Page 466; 691pp; English.
 XX
 CC The present invention relates to novel prostate-specific proteins (PSP)
 CC and their coding sequences. The PSPs and their coding sequences are
 CC useful for stimulating an immune response in a patient, or for treating
 CC prostate cancer in patient and for determining, detecting or diagnosing
 CC the presence of a cancer in a patient. The present sequence was used to
 CC illustrate the invention
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 116; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.9e-10; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 Qy 1 KENSAFPFCCNDNTAN 20
 Db 1 KENSAFPFCCNDNTAN 20
 RESULT 7
 ADB13955 ID ADB13955 standard; peptide; 20 AA.
 XX
 AC ADB13955;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DB Human prostate protein P503S epitope mapping peptide #2102.
 XX
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
 KW cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell; epitope.
 OS Homo sapiens.
 XX
 PN US2003185830-A1.
 XX
 PD 02-OCT-2003.
 XX
 PP 12-NOV-2002; 2002US-00294025.
 XX
 PR 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-0090804.
 PR 09-FEB-1998; 98US-00030956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159112.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00289346.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443386.
 PR 14-JAN-2000; 2000US-0048672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605733.
 PR 09-AUG-2000; 2000US-006651236.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657219.
 PR 02-OCT-2000; 2000US-00685166.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-0079729.
 PR 12-JAN-2001; 2001US-00759143.
 PR 09-FEB-2001; 2001US-00780669.
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-JUL-2001; 2001US-0095814.
 PR 09-MAY-2002; 2002US-00144678.

| | | |
|----|--|-----------------------------|
| XX | US2003157089-A1. | |
| PN | | |
| XX | | |
| PD | 21-AUG-2003. | |
| XX | | |
| PF | 09-MAY-2002; | 2000US-00144678. |
| XX | | |
| PR | 25-FEB-1997; | 97US-00806099 |
| PR | 01-AUG-1997; | 97US-00948034 |
| PR | 09-FEB-1998; | 98US-00020956 |
| PR | 25-FEB-1998; | 98US-00030607 |
| PR | 14-JUL-1998; | 98US-00115453 |
| PR | 23-SEP-1998; | 98US-00159812 |
| PR | 15-JAN-1999; | 99US-00232149 |
| PR | 09-APR-1999; | 99US-00288946 |
| PR | 13-JUL-1999; | 99US-00352616 |
| PR | 12-NOV-1999; | 99US-00439313 |
| PR | 18-NOV-1999; | 99US-00439368 |
| PR | 14-JAN-2000; | 2000US-00483677 |
| PR | 27-MAR-2000; | 2000US-00536857 |
| PR | 09-JAN-2000; | 2000US-00568100 |
| PR | 12-MAY-2000; | 2000US-00570737 |
| PR | 13-JUN-2000; | 2000US-00593793 |
| PR | 27-JUN-2000; | 2000US-00605783 |
| PR | 09-AUG-2000; | 2000US-00636215 |
| PR | 29-AUG-2000; | 2000US-00651236 |
| PR | 06-SEP-2000; | 2000US-00675279 |
| PR | 02-OCT-2000; | 2000US-00679446 |
| PR | 10-OCT-2000; | 2000US-00685166 |
| PR | 09-NOV-2000; | 2000US-00709729 |
| PR | 12-JAN-2001; | 2001US-00759133 |
| PR | 09-FEB-2001; | 2001US-00780669 |
| PR | 09-MAY-2001; | 2001US-00852911 |
| PR | 29-JUN-2001; | 2001US-00895814 |
| PR | 10-DEC-2001; | 2001US-00012896. |
| XX | | |
| PA | (CORIXA CORP. | |
| XX | | |
| PI | Xu J., Dillon DC, | Mitcham JL |
| PI | Kalos MD, | Fanger GR, |
| PI | Carter D, | Retter A, |
| PI | Li SX, | Wang A, |
| PI | Mcneill PD, | Vl |
| PI | Meagher MU, | Deng T; |
| XX | | |
| DR | WPI: 2003-777977/73. | |
| XX | | |
| PT | New polynucleotides encoding | human prostate tumor cDNA 1 |
| PT | a human prostate particularly prostate | cancer |
| XX | | |
| PS | Example 18; SEQ ID NO 505; 99 | |
| XX | | |
| CC | The invention relates to human | |
| CC | polynucleotides encoding them | |
| CC | antibody or its antigen-binding | |
| CC | polyptide of the invention, | |
| CC | comprising contacting a biolo- | |
| CC | gical binds a prostate-specific | |
| CC | bound polypeptide compared to | |
| CC | protein comprising a prostate | |
| CC | invention used to diagnose | |
| CC | cancer. This sequence represents | |
| CC | the invention. Note: The sequ- | |
| CC | ence of the printed specification | |
| CC | directly from USPTO at seqdat | |
| XX | Sequence 20 AA; | |
| SQ | | |

weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human microarrays, cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD4 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65105-ADR66514 represent the polynucleotide and polypeptide sequences used in the method of the invention.

Sequence 214 AA;

| | | | | | |
|----|-----------------------|-----------------|---------------|-----------|-------------|
| SQ | Query Match | 100.0% | Score 116; | DB 8; | Length 214; |
| | Best Local Similarity | 100.0% | Pred. No. 4 | 4e-09; | |
| | Matches 20; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

Qy 1 KENSAFPFCCNDNVTNTAN 20
Db 138 KENSAFPFCCNDNVTNTAN 157

RESULT 13

AAW75060
ID AAW75060 standard; protein; 233 AA.
XX DT 25-MAR-2003 (revised)
DT 28-JAN-1999 (first entry)

XX Human secreted protein encoded by gene 4 clone HKCSR70.
AC AAW75060;
XX

KW Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
KW Homo sapiens.

OS Homo sapiens.
XX
FH Key-Difference 233
FT Misc-difference /label= unknown

FT XX WO9839446-A2.
PN XX
PD 11-SEP-1998.
XX PF 06-MAR-1998; 9BWO-US004482.
XX 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07 MAR 1997; 97US-0040334P.
PR 07 MAR 1997; 97US-0040622P.
PR 11-APR-1997; 97US-0043311P.

XX PR 11-APR-1997; 97US-0043312P.
CC PR 11-APR-1997; 97US-0043313P.
CC PR 11-APR-1997; 97US-0043314P.
CC PR 11-APR-1997; 97US-0043315P.
CC PR 11-APR-1997; 97US-0043568P.
CC PR 11-APR-1997; 97US-0043569P.
CC PR 11-APR-1997; 97US-0043576P.
CC PR 11-APR-1997; 97US-0043578P.
CC PR 11-APR-1997; 97US-0043580P.
CC PR 11-APR-1997; 97US-0043669P.
CC PR 11-APR-1997; 97US-0043670P.
CC PR 11-APR-1997; 97US-0043671P.
CC PR 11-APR-1997; 97US-0043672P.
CC PR 11-APR-1997; 97US-0043674P.
CC PR 11-APR-1997; 97US-0043675P.
CC PR 11-APR-1997; 97US-0043676P.
CC PR 11-APR-1997; 97US-0043677P.
CC PR 11-APR-1997; 97US-0043678P.
CC PR 11-APR-1997; 97US-0043679P.
CC PR 11-APR-1997; 97US-0043680P.
CC PR 11-APR-1997; 97US-0043681P.
CC PR 11-APR-1997; 97US-0043682P.
CC PR 11-APR-1997; 97US-0043683P.
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CC PR 11-APR-1997; 97US-0043687P.
CC PR 11-APR-1997; 97US-0043688P.
CC PR 11-APR-1997; 97US-0043689P.
CC PR 11-APR-1997; 97US-0043690P.
CC PR 11-APR-1997; 97US-0043691P.
CC PR 11-APR-1997; 97US-0043692P.
CC PR 11-APR-1997; 97US-0043693P.
CC PR 11-APR-1997; 97US-0043694P.
CC PR 11-APR-1997; 97US-0043695P.
CC PR 11-APR-1997; 97US-0043696P.
CC PR 11-APR-1997; 97US-0043697P.
CC PR 11-APR-1997; 97US-0043698P.
CC PR 11-APR-1997; 97US-0043699P.
CC PR 11-APR-1997; 97US-0043700P.
CC PR 11-APR-1997; 97US-0043701P.
CC PR 11-APR-1997; 97US-0043702P.
CC PR 11-APR-1997; 97US-0043703P.
CC PR 11-APR-1997; 97US-0043704P.
CC PR 11-APR-1997; 97US-0043705P.
CC PR 11-APR-1997; 97US-0043706P.
CC PR 11-APR-1997; 97US-0043707P.
CC PR 11-APR-1997; 97US-0043708P.
CC PR 11-APR-1997; 97US-0043709P.
CC PR 11-APR-1997; 97US-0043710P.
CC PR 11-APR-1997; 97US-0043711P.
CC PR 11-APR-1997; 97US-0043712P.
CC PR 11-APR-1997; 97US-0043713P.
CC PR 11-APR-1997; 97US-0043714P.
CC PR 11-APR-1997; 97US-0043715P.
CC PR 11-APR-1997; 97US-0043716P.
CC PR 11-APR-1997; 97US-0043717P.
CC PR 11-APR-1997; 97US-0043718P.
CC PR 11-APR-1997; 97US-0043719P.
CC PR 11-APR-1997; 97US-0043720P.
CC PR 11-APR-1997; 97US-0043721P.
CC PR 11-APR-1997; 97US-0043722P.
CC PR 11-APR-1997; 97US-0043723P.
CC PR 11-APR-1997; 97US-0043724P.
CC PR 11-APR-1997; 97US-0043725P.
CC PR 11-APR-1997; 97US-0043726P.
CC PR 11-APR-1997; 97US-0043727P.
CC PR 11-APR-1997; 97US-0043728P.
CC PR 11-APR-1997; 97US-0043729P.
CC PR 11-APR-1997; 97US-0043730P.
CC PR 11-APR-1997; 97US-0043731P.
CC PR 11-APR-1997; 97US-0043732P.
CC PR 11-APR-1997; 97US-0043733P.
CC PR 11-APR-1997; 97US-0043734P.
CC PR 11-APR-1997; 97US-0043735P.
CC PR 11-APR-1997; 97US-0043736P.
CC PR 11-APR-1997; 97US-0043737P.
CC PR 11-APR-1997; 97US-0043738P.
CC PR 11-APR-1997; 97US-0043739P.
CC PR 11-APR-1997; 97US-0043740P.
CC PR 11-APR-1997; 97US-0043741P.
CC PR 11-APR-1997; 97US-0043742P.
CC PR 11-APR-1997; 97US-0043743P.
CC PR 11-APR-1997; 97US-0043744P.
CC PR 11-APR-1997; 97US-0043745P.
CC PR 11-APR-1997; 97US-0043746P.
CC PR 11-APR-1997; 97US-0043747P.
CC PR 11-APR-1997; 97US-0043748P.
CC PR 11-APR-1997; 97US-0043749P.
CC PR 11-APR-1997; 97US-0043750P.
CC PR 11-APR-1997; 97US-0043751P.
CC PR 11-APR-1997; 97US-0043752P.
CC PR 11-APR-1997; 97US-0043753P.
CC PR 11-APR-1997; 97US-0043754P.
CC PR 11-APR-1997; 97US-0043755P.
CC PR 11-APR-1997; 97US-0043756P.
CC PR 11-APR-1997; 97US-0043757P.
CC PR 11-APR-1997; 97US-0043758P.
CC PR 11-APR-1997; 97US-0043759P.
CC PR 11-APR-1997; 97US-0043760P.
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PR 22-AUG-1997; 97US-0056889P.
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 PR 22-AUG-1997; 97US-0056893P.
 PR 22-AUG-1997; 97US-0056894P.
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 PR 22-AUG-1997; 97US-0056911P.
 PR 05-SEP-1997; 97US-005750P.
 PR 05-SEP-1997; 97US-0057761P.
 XX (HUNA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Roben CA, Fischer CL, Soppet DR, Carter KC;
 PI Bednark DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
 PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 DR WPI: 1998-609887/51.
 DR N-PSDB; AAV34157.
 XX New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 disorders, immune diseases, inflammation or blood disorders.
 XX DR 1; Page 281-282; 47pp; English.
 XX This sequence represents a secreted human protein encoded by the gene
 clone detailed in the descriptor line. The gene can be used to generate
 fusion proteins by linking to the gene to a human immunoglobulin Fc
 portion (e.g. AAV34145) for increasing the stability of the fused protein
 as compared to the human protein only. The invention relates to 70 novel
 genes and their fragments (nucleic acid sequences: AAV34154-V341276; amino
 acid sequences AAV75057-W75179) which are useful for preventing, treating
 or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 pathological conditions can be diagnosed by determining the amount of the
 new polypeptides in a sample or by determining the presence of mutations
 in the new polynucleotides. Specific uses are described for each of the
 70 polynucleotides, based on which tissues they are most highly expressed
 in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
 PP Field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 233 AA;
 Query Match 100.0%; Score 116; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 4.8e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KENSAFPFFCNDNTNTAN 20
 Db 156 KENSAFPFFCNDNTNTAN 175
 SQ Sequence 233 AA;
 Query Match 100.0%; Score 116; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 4.8e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KENSAFPFFCNDNTNTAN 20
 Db 156 KENSAFPFFCNDNTNTAN 175
 RESULT 14
 ABO01936; ID ABO01936 standard; protein; 233 AA.
 XX AC ABO01936;
 XX DT 12-AUG-2003 (first entry)
 XX DE Novel human secreted protein #4.
 XX Human; immunoglobulin G; IgG; Fragment of crystallisation; Fc;
 KW immune system disorder; haematopoietic cell disorder;
 KW immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
 KW Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
 KW blood coagulation disorder; blood platelet disorder; autoimmune disorder;
 KW Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
 KW Glomerulonephritis; Grave's disease; allergic reaction;
 KW graft-versus-host disease; hyperproliferative disorder; neoplasm;
 KW infectious disease; nervous system disease; spinal cord disorder;

| | | | | |
|----|---|----------------|-----------------------|--|
| PR | 22-AUG-1997; | 97US-0056632P. | CC | (PS) fully defined in the specification and having biological activity, |
| PR | 22-AUG-1997; | 97US-0056636P. | CC | polypeptide domain or epitope of PS, secreted form of PS, full-length protein of PS, Or variant, allelic variant or species homologue of PS. |
| PR | 22-AUG-1997; | 97US-0056637P. | CC | (I) or a polynucleotide (II) encoding (I) is useful for preventing, (I) |
| PR | 22-AUG-1997; | 97US-0056662P. | CC | treating, or ameliorating a medical condition in a mammalian subject. (I) |
| PR | 22-AUG-1997; | 97US-0056664P. | CC | or (II) is also useful for diagnosing a pathological condition or a |
| PR | 22-AUG-1997; | 97US-0056685P. | CC | susceptibility to a pathological condition in a subject. (I) is useful |
| PR | 22-AUG-1997; | 97US-0056862P. | CC | for identifying a binding partner which involves contacting the |
| PR | 22-AUG-1997; | 97US-0056864P. | CC | polypeptide with the binding partner and determining whether the binding |
| PR | 22-AUG-1997; | 97US-0056872P. | CC | partner affects the activity of the polypeptide. (I) or (II) is useful |
| PR | 22-AUG-1997; | 97US-0056874P. | CC | for diagnosing or treating deficiencies or disorders of the immune |
| PR | 22-AUG-1997; | 97US-0056875P. | CC | system, deficiencies or disorders of haematopoietic cells, to treat |
| PR | 22-AUG-1997; | 97US-0056876P. | CC | immunologic deficiency disorders, ataxia telangiectasia, HIV infection, |
| PR | 22-AUG-1997; | 97US-0056877P. | CC | Wiskott-Aldrich disorders, thrombocytopoenia or haemoglobinuria, blood |
| PR | 22-AUG-1997; | 97US-0056878P. | CC | coagulation disorders, blood platelet disorders, autoimmune disorders |
| PR | 22-AUG-1997; | 97US-0056879P. | CC | (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis, |
| PR | 22-AUG-1997; | 97US-0056880P. | CC | dermatitis, glomerulonephritis, Grave's disease), allergic reactions, |
| PR | 22-AUG-1997; | 97US-0056881P. | CC | graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms |
| PR | 22-AUG-1997; | 97US-0056882P. | CC | located in the abdomen, bone, breast, digestive system, liver, pancreas, |
| PR | 22-AUG-1997; | 97US-0056884P. | CC | peritoneum, endocrine glands), infectious diseases (e.g., viral, |
| PR | 22-AUG-1997; | 97US-0056885P. | CC | bacterial, fungal or parasitic infection), central and peripheral nervous |
| PR | 22-AUG-1997; | 97US-0056887P. | CC | system diseases (e.g., spinal cord disorders, head trauma or stroke), to |
| PR | 22-AUG-1997; | 97US-0056889P. | CC | differentiate, proliferate and attract cells leading to the regeneration |
| PR | 22-AUG-1997; | 97US-0056890P. | CC | of tissues to repair, replace or protect tissue damaged by congenital |
| PR | 22-AUG-1997; | 97US-0056892P. | CC | defects, trauma (wounds, burns, incisions, or ulcers), age disease (e.g., |
| PR | 22-AUG-1997; | 97US-0056893P. | CC | osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV) |
| PR | 22-AUG-1997; | 97US-0056894P. | CC | is useful to modulate mammalian characteristics, to modulate mammalian |
| PR | 22-AUG-1997; | 97US-0056895P. | CC | metabolism affecting catabolism, anabolism, processing, utilisation, and |
| PR | 22-AUG-1997; | 97US-0056896P. | CC | storage of energy, to change a mammal's mental state or physical state, |
| PR | 22-AUG-1997; | 97US-0056909P. | CC | or as a food additive or preservative, such as to increase or decrease |
| PR | 22-AUG-1997; | 97US-0056910P. | CC | storage capabilities, fat content, lipid, protein, carbohydrate, |
| PR | 05-SEP-1997; | 97US-0056911P. | CC | vitamins, minerals, cofactors or other nutritional components. This is |
| PR | 05-SEP-1997; | 97US-0057650P. | CC | the amino acid sequence of a novel human secreted protein |
| PR | 06-MAR-1998; | 98WO-US004482. | XX | |
| XX | | | SQ | Sequence 233 AA; |
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| PA | (ROSE/) | ROSEN C A. | Best Local Similarity | 100.0% |
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| PA | (SDOP/) | SOPPET D R. | Conservative | 0; |
| PA | (CART/) | CARTER K C. | Mismatches | 0; |
| PA | (BEDDN/) | BEDNARIK D R. | Indels | 0; |
| PA | (ENDR/) | ENDRESS G A. | Gaps | 0; |
| PA | (YUJJ/) | YU G. | | |
| PA | (NIJUJ/) | NI J. | | |
| PA | (PEFNG/) | FENG P. | RESULT 15 | |
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| PA | (GREE/) | GREENE J M. | | |
| PA | (FERR/) | FERRIE A M. | XX | |
| PA | (DIUAN/) | DIUAN R. | XX | |
| PA | (HUOJ/) | HU J. | AC | AAG62153; |
| PA | (FLOR/) | FLORENCE K A. | XX | |
| PA | (OLSE/) | OLSEN H S. | XX | |
| PA | (EBNE/) | EBNER R. | XX | |
| PA | (BREW/) | BREWER L A. | XX | |
| PA | (SHIY/) | SHI Y. | XX | |
| XX | Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC; | KW | | |
| PI | Bednarik DR, Endress GR, Yu G, Ni J, Feng P, Young PE, Greene JM; | KW | | |
| PI | Perrine AM, duan R, Florence KA, Olsen HS, Ebner R, Brewer LA; | KW | | |
| PI | Shi Y. | KW | | |
| XX | WPI; 2003-466138/44. | KW | | |
| DR | N-PDB; ACD08028. | KW | | |
| XX | Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing | XX | | |
| PT | or treating deficiencies or disorders of the immune system, autoimmune | XX | | |
| PT | disorders, hyperproliferative disorders, and infectious diseases. | XX | | |
| XX | Claim 11; Page 173; 243DP; English. | XX | | |
| XX | The invention describes an isolated human secreted HODAZ50 polypeptide | XX | | |
| CC | (I) comprising a sequence at least 95% identical to a sequence selected | XX | | |
| CC | from polypeptide fragment of any one of the 123 polypeptide sequences | XX | | |
| PS | XX | | | |
| XX | Skeiky YAW, Xu J, Cheever MA, Reed SG; | XX | | |
| XX | WPI; 2001-328324/34. | DR | | |

XX Polypeptide comprising part of the Wilms Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WTI.
XX

PS Disclosure: Page 223-224; 228pp; English.

CC The present invention describes compositions comprising peptides derived
CC from the Wilms' tumour protein WTI and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WTI
CC proteins are provided. The human WTI gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a polypeptide described in the exemplification of the invention

SQ Sequence 240 AA;

| | | | | |
|-----------------------|--------|--------------|--------|---------------|
| Query Match | 100.0% | Score 116; | DB 4; | Length 240; |
| Best Local Similarity | 100.0% | Pred. No. | 5e-09; | |
| Matches | 20; | Conservative | 0; | Mismatches 0; |
| | | | | Indels 0; |
| | | | | Gaps 0; |

Qy 1 KENSAFPPFCNDNVNTAN 20
Db 165 KENSAFPPFCNDNVNTAN 184

Search completed: February 5, 2005, 19:59:55
Job time : 104.746 secs

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OM protein - protein search, using sw model

Run on: February 5, 2005, 20:00:18 ; Search time 74.9153 Seconds
(without alignments)
86.952 Million cell updates/sec

Title: US-09-780-669-114_COPY_165_184

Perfect score: 116

Sequence: 1 KENSAFFPCCNDNVNTAN 20

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|----------------------------|--------------------|
| 1 | 116 | 100.0 | 20 9 US-09-759-143-505 | Sequence 505, APP |
| 2 | 116 | 100.0 | 20 9 US-09-780-669-505 | Sequence 505, APP |
| 3 | 116 | 100.0 | 20 9 US-09-822-827-505 | Sequence 505, APP |
| 4 | 116 | 100.0 | 20 9 US-09-895-793-505 | Sequence 505, APP |
| 5 | 116 | 100.0 | 20 9 US-09-895-814-505 | Sequence 505, APP |
| 6 | 116 | 100.0 | 20 13 US-10-012-896-505 | Sequence 505, APP |
| 7 | 116 | 100.0 | 20 14 US-10-010-940-505 | Sequence 505, APP |
| 8 | 116 | 100.0 | 20 14 US-10-144-678A-505 | Sequence 505, APP |
| 9 | 116 | 100.0 | 20 14 US-10-294-025-505 | Sequence 505, APP |
| 10 | 116 | 100.0 | 233 9 US-09-981-876-137 | Sequence 137, APP |
| 11 | 116 | 100.0 | 233 10 US-09-148-545-137 | Sequence 137, APP |
| 12 | 116 | 100.0 | 240 15 US-10-264-237-1489 | Sequence 1489, APP |
| 13 | 116 | 100.0 | 241 9 US-09-759-143-114 | Sequence 114, APP |
| 14 | 116 | 100.0 | 241 9 US-09-780-669-114 | Sequence 114, APP |
| 15 | 116 | 100.0 | 241 9 US-09-822-827-114 | Sequence 114, APP |
| 16 | 116 | 100.0 | 241 9 US-09-115-853-114 | Sequence 114, APP |
| 17 | 116 | 100.0 | 241 9 US-09-232-880-114 | Sequence 114, APP |
| 18 | 116 | 100.0 | 241 9 US-09-895-793-114 | Sequence 114, APP |
| 19 | 116 | 100.0 | 241 9 US-09-895-814-114 | Sequence 114, APP |
| 20 | 116 | 100.0 | 241 9 US-09-895-814-114 | Sequence 114, APP |
| 21 | 116 | 100.0 | 241 9 US-09-895-814-114 | Sequence 114, APP |
| 22 | 116 | 100.0 | 241 13 US-10-012-896-114 | Sequence 114, APP |
| 23 | 116 | 100.0 | 241 14 US-10-097-340-126 | Sequence 326, APP |
| 24 | 116 | 100.0 | 241 14 US-10-010-940-114 | Sequence 114, APP |
| 25 | 116 | 100.0 | 241 14 US-10-205-823-125 | Sequence 425, APP |
| 26 | 116 | 100.0 | 241 14 US-10-144-678A-114 | Sequence 114, APP |
| 27 | 116 | 100.0 | 241 14 US-10-205-823-123 | Sequence 423, APP |
| 28 | 116 | 100.0 | 241 14 US-10-295-027-104 | Sequence 20, APP |
| 29 | 116 | 100.0 | 241 15 US-10-037-417-77 | Sequence 77, APP |
| 30 | 116 | 100.0 | 241 15 US-10-037-417-78 | Sequence 78, APP |
| 31 | 116 | 100.0 | 241 16 US-10-688-838-114 | Sequence 114, APP |
| 32 | 116 | 100.0 | 258 14 US-10-097-340-124 | Sequence 324, APP |
| 33 | 116 | 100.0 | 258 14 US-10-205-823-123 | Sequence 423, APP |
| 34 | 116 | 100.0 | 273 14 US-10-156-136-40 | Sequence 20, APP |
| 35 | 50 | 43.1 | 92 16 US-10-437-963-89981 | Sequence 18981, |
| 36 | 50 | 43.1 | 240 9 US-09-908-193-43 | Sequence 43, APP |
| 37 | 50 | 43.1 | 240 10 US-09-823-187-74 | Sequence 74, APP |
| 38 | 50 | 43.1 | 240 15 US-10-037-417-76 | Sequence 76, APP |
| 39 | 50 | 43.1 | 241 15 US-10-037-417-22 | Sequence 22, APP |
| 40 | 50 | 43.1 | 301 15 US-10-299-867-21 | Sequence 21, APP |
| 41 | 50 | 43.1 | 544 16 US-10-450-156-1 | Sequence 1, APP |
| 42 | 48 | 41.4 | 49 9 US-09-864-761-39257 | Sequence 39257, A |
| 43 | 47 | 40.5 | 165 15 US-10-424-599-49829 | Sequence 249829, |
| 44 | 46.5 | 40.1 | 74 14 US-10-316-253-38 | Sequence 58, APP |
| 45 | 46.5 | 40.1 | 1887 10 US-09-853-180-3 | Sequence 3, APP |

ALIGNMENTS

RESULT 1
US-09-759-143-505

; Sequence 505, Application US/03759143 .
 ; Patent No. US2002002248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: XU, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlicker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalocs, Michael D.
 ; APPLICANT: Ranger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Veddick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Li, Samu
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121-427C23
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 505
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 ; US-09-759-143-505

Query Match 100.0%; Score 116; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 SEQ ID NO: 505
 US-09-780-669-114
 Sequence 505, Application US/09780669
 Patent No. US20020051977A1

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 Query Match 100.0%; Score 116; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 SEQ ID NO: 505
 US-09-780-669-114
 Sequence 505, Application US/09780669
 Patent No. US20020051977A1

GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqui
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Day, Craig H.
 APPLICANT: Stolk, John A.
 APPLICANT: Vediick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 APPLICANT: Hurai, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121-427C24
 CURRENT APPLICATION NUMBER: US/09/780,669
 CURRENT FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 943
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 505
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Made in a lab
 US-09-780-669-505

Query Match 100.0%; Score 116; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 SEQ ID NO: 505
 US-09-780-669-114
 Sequence 505, Application US/09780669
 Patent No. US20020051977A1

GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121-534C1
 CURRENT APPLICATION NUMBER: US/09/822,827
 CURRENT FILING DATE: 2001-03-28
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 505

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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 SEQ ID NO: 505
 US-09-895-793-505
 Sequence 505, Application US/09895793
 Publication No. US20020192763A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqui
 APPLICANT: Kalos, Michael D.
 APPLICANT: Rettner, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William T.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Hurai, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Vinals de Bassols, Carlota
 APPLICANT: Foy, Teresa
 APPLICANT: Fanger, Gary R.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121-534C2
 CURRENT APPLICATION NUMBER: US/09/895,793
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 505

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 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 SEQ ID NO: 505
 US-09-895-793-505
 Sequence 505, Application US/09895793
 Publication No. US20020192763A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121-534C1
 CURRENT APPLICATION NUMBER: US/09/822,827
 CURRENT FILING DATE: 2001-03-28
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 505

RESULT 5
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 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: Made in a lab
 SEQ ID NO: 505
 US-09-895-814-505
 Sequence 505, Application US/09895793
 Publication No. US20020192763A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yiqiu
 APPLICANT: Kalos, Michael D.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Ajun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William T.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Rural, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Vinals de Bassols, Carlota
 APPLICANT: Foy, Teresa
 APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.427C26
 CURRENT APPLICATION NUMBER: US/09/895, 814
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 990

SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 505
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 ; OTHER INFORMATION: Made in a lab

US-09-895-814-505

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 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 KENSAFPFCCNDNTNTAN 20

RESULT 6
 US-10-012-896-505
 ; Sequence 505, Application US/10012896
 ; Publication No. US20020183251A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yiqiu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Rural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Wanatabe, Yoshihiro

; APPLICANT: Meagher, Madeleine Joy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C27
 ; CURRENT APPLICATION NUMBER: US/10/012, 896
 ; NUMBER OF SEQ ID NOS: 1011
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 505
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab

US-10-012-896-505

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 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 KENSAFPFCCNDNTNTAN 20

RESULT 7
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 ; Sequence 505, Application US/10010940
 ; Publication No. US20030088062A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Jiang, Yiqui
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael E.
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solt, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427D3
 ; CURRENT APPLICATION NUMBER: US/10/010, 940
 ; CURRENT FILING DATE: 2001-12-05
 ; NUMBER OF SEQ ID NOS: 575
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 505
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab

US-10-010-940-505

Query Match 100.0%; Score 116; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAFPFCCNDNTNTAN 20
 Db 1 KENSAFPFCCNDNTNTAN 20

RESULT 8
 US-10-144-678A-505
 ; Sequence 505, Application US/10144678A
 ; Publication No. US20030157089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.

RESULT 10
 US-09-981-876-137
 ; Sequence 137, Application US/0981876
 ; Patent No. US20020164669A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 70 Human Secreted Proteins
 ; CURRENT APPLICATION NUMBER: US/09/981,876
 ; CURRENT FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: 09/148,545
 ; PRIOR FILING DATE: 1998-09-04
 ; FILE REFERENCE: PZ001P1
 ; PRIOR APPLICATION NUMBER: 60/040,162
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/040,333
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/038,621
 ; PRIOR FILING DATE: 1997-03-07
 ; PRIOR APPLICATION NUMBER: 60/040,161
 ; PRIOR FILING DATE: 1997-03-07
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 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,596
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,612
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 60/047,632

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 Best Local Similarity 100.0% Pred. No. 1.3e-0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 KENSAFPFCCNDNVTNTAN 20

RESULT 9
 US-10-224-025-505
 ; Sequence 505, Application US/10294025
 ; Publication No. US20030185030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C29
 ; CURRENT APPLICATION NUMBER: US/10/294,025
 ; CURRENT FILING DATE: 2003-11-12
 ; NUMBER OF SEQ ID NOS: 1038
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 505
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: Made in a lab

Query Match 100.0% Score 116; DB 14; Length 20;
 Best Local Similarity 100.0% Pred. No. 1.3e-0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAFPFCCNDNVTNTAN 20

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PRIORITY APPLICATION NUMBER: 60/0056, 892
PRIORITY FILING DATE: 1997-08-22
PRIORITY APPLICATION NUMBER: 60/0047, 595
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/0057, 761
PRIORITY FILING DATE: 05-Sep-1997
PRIORITY APPLICATION NUMBER: 60/0047, 588
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/0047, 585
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PRIORITY APPLICATION NUMBER: 60/0047, 589
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/0047, 593
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/0047, 614
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/0043, 578
PRIORITY FILING DATE: 1997-04-11
PRIORITY APPLICATION NUMBER: 60/0043, 576
PRIORITY FILING DATE: 1997-04-11
PRIORITY APPLICATION NUMBER: 60/0047, 501
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/0043, 670
PRIORITY FILING DATE: 1997-04-11
PRIORITY APPLICATION NUMBER: 60/0056, 632
PRIORITY FILING DATE: 1997-08-22
PRIORITY APPLICATION NUMBER: 60/0056, 664
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PRIORITY FILING DATE: 1997-06-06
PRIORITY APPLICATION NUMBER: 60/0057, 650
PRIORITY FILING DATE: 1997-09-05
PRIORITY APPLICATION NUMBER: 60/0056, 884
PRIORITY FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 137
LENGTH: 233
;
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Publication No. US20030027132A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001LP1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
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; EARLIER APPLICATION NUMBER: 60/047,583
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; EARLIER APPLICATION NUMBER: 60/047,617
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
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; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568

EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
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EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
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EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-05
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-12
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 05-Sep-1997
EARLIER APPLICATION NUMBER: 60/047,599

; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,588
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,585
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,586
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,590
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,594
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,589
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,593
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,614
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/043,578
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,576
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/047,501
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/043,670
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/056,632
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,664
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,876
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,881
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,909
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,875
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,862
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,887
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,908
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/048,964
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/056,884
 ; EARLIER FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 280
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 137
 ; LENGTH: 233

Query Match 100.0%; Score 116; DB 10; Length 233;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAFPFCCNDNTNTAN 20
 Db 156 KENSAFPFCCNDNTNTAN 175

RESULT 12

US-10-264-237-1489
 ; Sequence 1489, Application US/10264237
 ; PUBLICATION NO. US20040009491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA131P1
 ; CURRENT APPLICATION NUMBER: US/10/264,237
 ; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: PCT/US01/16450
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: US 60/205,515
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 2876
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO: 1489
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-264-237-1489

Query Match 100.0%; Score 116; DB 15; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAFPFCCNDNTNTAN 20
 Db 164 KENSAFPFCCNDNTNTAN 183

RESULT 13

US-09-759-143-114

; Sequence 114, Application US/09759143
 ; Patent No. US200502248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121427C23
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; CURRENT FILING DATE: 2005-01-12
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSEQ For Windows Version 3.0
 ; SEQ ID NO: 114
 ; LENGTH: 241

Query Match 100.0%; Score 116; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAFPFCCNDNTNTAN 20
 Db 165 KENSAFPFCCNDNTNTAN 184

RESULT 14

US-09-780-669-114

; Sequence 114, Application US/09780669
 ; Patent No. US200505977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Ajun
 APPLICANT: Sheiky, Yasir A.W.
 APPLICANT: Hepler, William
 APPLICANT: Hural, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 211121-427C24
 CURRENT APPLICATION NUMBER: US/09/780,669
 CURRENT FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 943
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 114
 LENGTH: 241
 TYPE: PRF
 ORGANISM: Homo sapien
 US-09-780-669-114

Query Match 100.0%; Score 116; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 KENSAFPFPCCNDNTAN 20
 Db 165 KENSAFPFPCCNDNTAN 184

RESULT 15
 US-09-030-606-114
 Sequence 114, Application US/09030606
 Patent No. US2002008150A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 STREET: SEED and BERRY LLP
 CITY: 6300 Columbia Center, 701 Fifth Avenue
 STATE: Seattle
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/030,606
 FILING DATE: 25-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE DOCKET NUMBER: 210121-428C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 114:
 SEQUENCE CHARACTERISTICS:

| | | | | | | | | |
|--|--------------------------------|--|--------|-----------|--|-----------------------|-----------------------------|----------|
| protein - protein search, using SW model | | | | | | | | |
| on: | February 5, 2005, 19:49:45 ; | Search time 19.661 Seconds (without alignments) | | | | | | |
| | | 97.876 Million cell updates/sec | | | | | | |
| file: | US-09-780-669-114_COPY_165_184 | | | | | | | |
| effect score: | 116 | | | | | | | |
| source: | 1 KENSAFPPFCNDNTANTAN 20 | | | | | | | |
| string table: | BLOSUM62 | | | | | | | |
| Gapopen: | Gapext 10.0 , Gapext 0.5 | | | | | | | |
| searched: | 283416 seqs, 96216763 residues | | | | | | | |
| total number of hits satisfying chosen parameters: | 283416 | | | | | | | |
| minimum DB seq length: | 0 | | | | | | | |
| maximum DB seq length: | 2000000000 | | | | | | | |
| t-processing: Minimum Match 0% | Maximum Match 100% | | | | | | | |
| Listing first 45 summaries | | | | | | | | |
| database : | PIR-79;* | | | | | | | |
| | 1: Pir1;* | | | | | | | |
| | 2: Pir2;* | | | | | | | |
| | 3: Pir3;* | | | | | | | |
| | 4: Pir4;* | | | | | | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution. | | | | | | | | |
| SUMMARIES | | | | | | | | |
| | | | | | | | | |
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| 1 | 116 | 100.0 | 241 | 2 A59262 | tetrapsan TSPAN-1 | Query | 1 KENSAFPPFCNDNTANTAN 20 | RESULT 1 |
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| 3 | 51 | 44.0 | 860 | 1 VCLwB4 | env polyprotein pr | Matches | 0; Mismatches 0; | |
| 4 | 50 | 43.1 | 301 | 2 S7591 | prophage methionyl | Indels | 0; | |
| 5 | 50 | 43.1 | 566 | 2 S1907 | carboxylesterase (| Gaps | | |
| 6 | 48 | 41.4 | 1293 | 2 S4202 | xeroderma pigmento | | | |
| 7 | 46 | 39.7 | 194 | 2 P64598 | modulator of drug | | | |
| 8 | 46 | 39.7 | 633 | 2 T04179 | hypothetical prote | | | |
| 9 | 46 | 39.7 | 859 | 1 VCLwJ22 | env polyprotein pr | | | |
| 10 | 46 | 39.7 | 859 | 1 VCLwB1 | env polyprotein pr | | | |
| 11 | 46 | 39.7 | 859 | 1 VCLwB2 | env polyprotein pr | | | |
| 12 | 46 | 39.7 | 859 | 1 VCLwJ3 | env polyprotein pr | | | |
| 13 | 46 | 39.7 | 859 | 1 VCLwJ4V | env polyprotein pr | | | |
| 14 | 46 | 39.7 | 859 | 1 VCLwJEW | env polyprotein pr | | | |
| 15 | 46 | 39.7 | 859 | 1 VCLwJ1 | hypothetical prote | | | |
| 16 | 45 | 38.8 | 128 | 2 T15101 | hypothetical prote | | | |
| 17 | 45 | 38.8 | 145 | 2 T49228 | cyclin-dependent k | | | |
| 18 | 45 | 38.8 | 196 | 2 T09568 | NADH dehydrogenas | | | |
| 19 | 45 | 38.8 | 460 | 2 C7311 | B. subtilis ynd P | | | |
| 20 | 45 | 38.8 | 463 | 2 A11744 | hypothetical prote | | | |
| 21 | 44.5 | 38.4 | 218 | 2 T34373 | first-mannosidase I | | | |
| 22 | 44.5 | 38.4 | 363 | 2 F6925 | probable phosphoch | | | |
| 23 | 44 | 37.9 | 279 | 2 B71415 | probable phosphoch | | | |
| 24 | 44 | 37.9 | 298 | 2 E85166 | transcription fact | | | |
| 25 | 44 | 37.9 | 996 | 2 S70446 | conserved hypothet | | | |
| 26 | 43 | 37.1 | 68 | 2 AB0417 | hypothetical prote | | | |
| 27 | 43 | 37.1 | 194 | 2 A71915 | probable endopept | | | |
| 28 | 43 | 37.1 | 241 | 2 S12375 | coot protein type: DNA | | | |
| 29 | 43 | 37.1 | 304 | 2 S12376 | A; Residues: 1-108 | | | |
| | | | | | A; Status: Preliminary | | | |
| | | | | | C; Species: Neurospora crassa | | | |
| | | | | | N; Alternate names: blue-light-inducible protein bli-7 | | | |
| | | | | | C; Species: Neurospora crassa | | | |
| | | | | | C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 | | | |
| | | | | | C; Accession: A46222; A56345 | | | |
| | | | | | R; Bell-Pedersen, D.; Dunlap, J.C.; Loros, J.J. | | | |
| | | | | | Genes Dev. 6, 2382-2394, 1992 | | | |
| | | | | | A; Title: The Neurospora circadian clock-controlled gene, <i>ccg-2</i> , is allelic to | | | |
| | | | | | A; Reference: A46222; PMID: 1459460 | | | |
| | | | | | A; Accession: A46222 | | | |
| | | | | | A; Status: Preliminary | | | |
| | | | | | R; Ebnerle, J.; Russo, V.E. | | | |
| | | | | | DNA Seq. 3, 131-141, 1992 | | | |
| | | | | | A; Title: Neurospora crassa blue-light-inducible gene bli-7 encodes a short hyd | | | |
| | | | | | A; Reference number: A56645; PMID: 1472707 | | | |
| | | | | | A; Accession: A56645 | | | |
| | | | | | A; Molecule type: DNA | | | |
| | | | | | A; Residues: 1-108 | | | |

A;Cross-references: GB:X62170; GB:SS51408; NID:9296383; PID:CAA44101.1; PMID:g296384

A;Note: sequence extracted from NCBI backbone (NCBIN:121427, NCBBP:121428)

C;Genetics: A/Genes: bli-7; ccg-2

Query Match 44.0%; Score 51; DB 2; Length 108;

Best Local Similarity 72.7%; Pred. No. 1.4; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 8; Query Match 10 CCND1NTNTAN 20

Db 86 CCKDDVNTGN 96

RESULT 3

VCLJE4

env polyprotein precursor (clone P3.2-5) - equine infectious anemia virus

C;Species: coat protein gp15; coat protein gp90

C;Species: equine infectious anemia virus

A;Note: host Equus caballus (domestic horse)

A;Accession: D34027

C;Sequence-revision: 31-Mar-1991 #text_change 09-Jul-2004

R;Payne, S.L.; Pang, F.D.; Liu, C.P.; Dhruva, B.R.; Rwambo, P.; Issel, C.J.; Montelaro, C;Genetics:

A;Title: Antigenic variation and lentivirus persistence: variations in envelope gene seq

A;Reference number: A34027; PMID:88072070; PMID:2825406

A;Accession: D34027

A;Molecule type: Genomic RNA

A;Residues: 1-860 <PAY>

A;Cross-references: UNIPROT:P224310; GB:MI18388; NID:g323841; PID:AAA66410.1; PMID:g333842

C;Genetics:

A;Gene: env

C;Keywords: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-445/Product: coat protein y990 #status predicted <CP1>

F;75-93/Domain: transmembrane #status predicted <TM1>

F;446-860/Product: coat protein q945 #status predicted <CP2>

F;447-463/Domain: transmembrane #status predicted <TM2>

F;615-637/Domain: transmembrane #status predicted <TM3>

F;788-808/Domain: transmembrane #status predicted <TM4>

F;817-836/Domain: transmembrane #status predicted <TM5>

F;40.112.141.148.186.214.235.244.308.337.340.346.369.400.407.412.423.484.491.551.558

Query Match 44.0%; Score 51; DB 1; Length 860;

Best Local Similarity 44.4%; Pred. No. 8.7; Mismatches 5; Indels 0; Gaps 0;

Matches 8; Conservative 8; Query Match 1 KENSAFPFPCCNDNTNT 18

Db 28 EENTTFOQYCNNSKNS 45

RESULT 4

S75391

Probable methionyl aminopeptidase (EC 3.4.11.18) - Sulfolobus solfataricus

C;Alternative names: protein C04024; translation initiation factor eifR-2-associated protei

C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C;Accession: S75391

R;Sensen, C.W.; Kleck, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.

Mol Microbiol 22, 175-191, 1996

A;Title: Organizational characteristics and information content of an archaeal genome: 1

A;Reference number: 973076; PMID:8899719

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Cross-references: UNIPROT:P95963; EMBL:Y08257; NID:91707772; PID:CAA65553.1; PMID:g170

A;Experimental source: strain P2

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996

C;Superfamily: Escherichia coli methionyl aminopeptidase

C;Keywords: aminopeptidase

Query Match 43.1%; Score 50; DB 2; Length 301;

Best Local Similarity 50.0%; Pred. No. 4.8; Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 2 ENSAPPFPCCNDNTNTA 19

Db 46 ENKAFFSPPNISNSEA 63

RESULT 5

S19307

carboxylesterase (EC 3.1.1.1) precursor - pig

N;Alternate name: proline-beta-naphthyl amidase

C;Species: Sus scrofa domesticus (domestic pig)

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004

C;Accession: S19307; PMID:92607

R;Macauschima, M.; Iriue, H.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Takahashi

PEBS Lett. 293, 37-41, 1991

A;Title: The nucleotide and reduced amino acid sequences of porcine liver proline-beta-n

A;Reference number: S19307; PMID:1959668

A;Accession: S19307

A;Molecule type: mRNA

A;Cross-references: UNIPROT:Q29550; EMBL:X63323; NID:91930; PID:CAA44929.1; PMID:g1931

A;Accession: S207071; PMID:1959668

A;Molecule type: protein

A;Residues: 19-40 <PAT2>

A;Note: 2-Lys and 33-Leu were also found

C;Superfamily: cholinesterase; cholinesterase homology

C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer

F;1-18/Domain: signal sequence #status Predicted <SIG>

F;19-566/Product: carboxylesterase #status experimental <WAT>

F;51-552/Domain: cholinesterase homology <CHB>

F;80/Binding site: carbohydrate (asn) (covalent) #status predicted

F;80/Binding site: Ser, His #status predicted

Query Match 43.1%; Score 50; DB 2; Length 566;

Best Local Similarity 46.7%; Pred. No. 8.4; Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 1 KENSAFPFPCCNDNT 15

Db 79 KNTTSYPPMCCQDPV 93

RESULT 6

S2402

xeroderma pigmentosum group C complementing factor - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S42402; PMID:929259

R;Henning, K.A.; Peterson, C.; Legerski, R.; Friedberg, E.C.

Nucleic Acids Res. 22, 257-261, 1994

A;Title: Cloning the Drosophila homolog of the xeroderma pigmentosum complementation gro

A;Reference number: S42402; PMID:94173669; PMID:8127661

A;Accession: S42402

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1233 <HEH>

A;Cross-references: UNIPROT:Q24595; EMBL:Z28622; NID:9434007; PID:CAA82262.1; PMID:g170

A;Genetic: Flybase:XPc

A;Cross-references: FlyBase:FBgn0004698

Query Match 41.4%; Score 48; DB 2; Length 1293;

Best Local Similarity 45.0%; Pred. No. 35; Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 1 KENSAFPFPCCNDNTANT 20

Db 166 KEKSPAPQFDNCAGTINLSD 185

RESULT 7

P64598
modulator of drug activity - *Helicobacter pylori* (strain 26695)
C;Species: *Helicobacter pylori*
C;Date: 09-Aug-1997 #text_change 09-Aug-1997 #text_revision 09-Jul-2004
C;Accession: P64598
R;Tomb, J.P.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, C.,
A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A;Reference number: A64522; PMID:9739467; PMID:9452185
A;Accession: F64598
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-194 <ROM>
A;Cross-references: UNIPROT:O25347; GB:AE000577; GB:AE000511; NID:g2313747; PIDN:AA0769
C;Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match 39.7%; Score 46; DB 2; Length 194;

Best Local Similarity 64.3%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 10

VCLJBL

env polyprotein precursor (clone P3-2-1) - equine infectious anemia virus

N;Contains: coat protein gp45; coat protein gp90

C;Species: equine infectious anemia virus

A;Note: host Equus caballus (domestic horse)

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C;Accession: A34027

A;Molecule type: genomic RNA

A;Residues: 1-859 <PAY>

A;Cross-references: UNIPROT:P22427; GB:MI18385; NID:g323830; PIDN:AAA66407.1; PMID:g323831

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; Glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

C;Superfamily: equine infectious anemia virus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-859/Domain: env polyprotein #status predicted <ENV>

F;23-444/Product: coat protein gp90 #status predicted <GPP>

F;445-859/Product: coat protein gp45 #status predicted <GPP>

F;446-472/Region: hydrophobic

F;615-636/Domain: transmembrane #status predicted <TMN>

F;40,112,141,148,186,214,233,244,340,368,393,406,411,483,490,550,557/Binding site: carbo

PIDN:AAA43005.1; PMID:g290630

A;Cross-references: UNIPROT:Q929627; GB:M87581; NID:g290627; PIDN:AAA43005.1; PMID:g290630

C;Genetics:

A;Gene: env

| | |
|--|--|
| A;Title: Antigenic variation and lentivirus persistence: variations in envelope gene seq | |
| A;Reference number: A34027; MUID:88072070; PMID:2823406. | |
| A;Accession: B34027 | |
| A;Molecule type: genomic RNA | |
| A;Residues: 1-859 <PA> | |
| A;Cross-references: UNIPROT:P22428; GB:M18386; NID:9323832; PIDN:AAA66408_1; PID:9323833 | |
| C;Genetics: | |
| A;Gene: env | |
| C;Superfamily: equine infectious anemia virus env polyprotein | |
| C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein | |
| F;1-22/Domain: signal sequence #status predicted <SIG> | |
| F;23-44/Product: coat protein gp90 #status predicted <CP1> | |
| F;75-93/Domain: transmembrane #status predicted <TM1> | |
| F;445-859/Product: coat protein gp45 #status predicted <CP2> | |
| F;446-462/Domain: transmembrane #status predicted <TM2> | |
| F;614-636/Domain: transmembrane #status predicted <TM3> | |
| F;787-807/Domain: transmembrane #status predicted <TM4> | |
| F;816-835/Domain: transmembrane #status predicted <TM5> | |
| F;40,112-141,148,184,201,214,233,244,313,340,346,368,399,406,411,422,483,490,550,557 | |
| Query Match 39.7%; Score 46; DB 1; Length 859; | |
| Best Local Similarity 38.9%; Pred. No. 48; | |
| Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0; | |
| Qy 1 KENSAFPPFCNDVNTNT 18 | |
| Db : : : : : : | |
| 28 EENTMFQPYCYNNDSKNS 45 | |
| RESULT 12 | |
| VCLJE3 | |
| env polyprotein precursor (clone P3-2-3) - equine infectious anemia virus | |
| N;Contains: coat protein gp45; coat protein gp90 | |
| C;Species: equine infectious anemia virus | |
| A;Note: host Equus caballus (domestic horse) | |
| C;Accession: C34027 | |
| R.Payne, S.L.; Fang, F.D.; Liu, C.P.; Dhruva, B.R.; Issel, C.J.; Montelaro, Virology, 161, 322-331, 1987 | |
| A;Title: Antigenic variation and lentivirus persistence: variations in envelope gene seq | |
| A;Reference number: A34027; MUID:88072070; PMID:2825406 | |
| A;Accession: C34027 | |
| A;Molecule type: genomic RNA | |
| A;Residues: 1-859 <PA> | |
| A;Cross-references: UNIPROT:P22429; GB:M18387; NID:9323834; PIDN:AAA66409_1; PID:9323835 | |
| C;Genetics: | |
| A;Gene: env | |
| C;Superfamily: equine infectious anemia virus env polyprotein | |
| C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein | |
| F;1-22/Domain: signal sequence #status predicted <SIG> | |
| F;23-44/Product: coat protein gp90 #status predicted <CP1> | |
| F;75-93/Domain: transmembrane #status predicted <TM1> | |
| F;445-859/Product: coat protein gp45 #status predicted <CP2> | |
| F;614-636/Domain: transmembrane #status predicted <TM2> | |
| F;787-807/Domain: transmembrane #status predicted <TM3> | |
| F;816-835/Domain: transmembrane #status predicted <TM4> | |
| F;40,112-141,148,186,214,233,244,313,340,346,368,399,406,411,422,483,490,550,557,752/Binding site | |
| Query Match 39.7%; Score 46; DB 1; Length 859; | |
| Best Local Similarity 38.9%; Pred. No. 48; | |
| Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0; | |
| Qy 1 KENSAFPPFCNDVNTNT 18 | |
| Db : : : : : : : | |
| 28 EENTMFQPYCYNNDSKNS 45 | |
| RESULT 13 | |
| VCLJEF | |
| env polyprotein precursor - equine infectious anemia virus | |
| N;Contains: coat protein gp45; coat protein gp90 | |
| C;Species: equine infectious anemia virus | |
| A;Note: host Equus caballus (domestic horse) | |
| C;Accession: C34027 | |
| R.Payne, S.L.; Fang, F.D.; Liu, C.P.; Dhruva, B.R.; Issel, C.J.; Montelaro, Virology, 161, 322-331, 1987 | |
| A;Title: Antigenic variation and lentivirus persistence: variations in envelope gene seq | |
| A;Reference number: A34027; MUID:88072070; PMID:2825406 | |
| A;Accession: C34027 | |
| A;Molecule type: genomic RNA | |
| A;Residues: 1-859 <PA> | |
| A;Cross-references: UNIPROT:P22429; GB:M18387; NID:9323834; PIDN:AAA66409_1; PID:9323835 | |
| C;Genetics: | |
| A;Gene: env | |
| C;Superfamily: equine infectious anemia virus env polyprotein | |
| C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein | |
| F;1-22/Domain: signal sequence #status predicted <SIG> | |
| F;23-44/Product: coat protein gp90 #status predicted <CP1> | |
| F;75-93/Domain: transmembrane #status predicted <TM1> | |
| F;445-859/Product: coat protein gp45 #status predicted <CP2> | |
| F;614-636/Domain: transmembrane #status predicted <TM2> | |
| F;787-807/Domain: transmembrane #status predicted <TM3> | |
| F;816-835/Domain: transmembrane #status predicted <TM4> | |
| F;40,112-141,148,186,214,233,244,313,340,346,368,399,406,411,422,483,490,550,557,752/Binding site | |
| Query Match 39.7%; Score 46; DB 1; Length 859; | |
| Best Local Similarity 38.9%; Pred. No. 48; | |
| Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0; | |
| Qy 1 KENSAFPPFCNDVNTNT 18 | |
| Db : : : : : : : | |
| 28 EENTMFQPYCYNNDSKNS 45 | |

A1:Note: host: *Equis caballus* (domestic horse)
 A1:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
 C1:Accession: A25610 #B25610
 C1:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 C1:Superfamily: equine infectious anemia virus env polyprotein
 C1:Domain: signal sequence #status Predicted <SIG>
 F1:23-444/Product: coat protein gp90 #status Predicted <GPP>
 F1:45-859/Product: coat protein gp45 #status Predicted <GPP>
 F1:46-472/Domain: transmembrane #status Predicted <TM>
 F1:617-636/Domain: transmembrane #status Predicted <TMN>
 F1:40,112,141,148,186,214,233,244,340,368,399,406,411,483,490,550,557,752/Bis
 A1:Reference number: A25610; MUID:87071653; PMID:2431539
 A1:Accession: A25610
 A1:Molecule type: DNA
 A1:Residues: 1-859 <RUS>
 A1:Cross-references: UNIPROT:P06751
 C1:Genetics:
 A1:Gene: env
 C1:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 C1:Superfamily: equine infectious anemia virus env polyprotein
 C1:Domain: signal sequence #status Predicted <SIG>
 F1:23-444/Product: coat protein gp90 #status Predicted <GPP>
 F1:45-859/Product: coat protein gp45 #status Predicted <GPP>
 F1:46-472/Domain: transmembrane #status Predicted <TM>
 F1:617-636/Domain: transmembrane #status Predicted <TMN>
 F1:40,112,141,148,186,214,233,244,340,368,399,406,411,483,490,550,557,752/Bis
 Query Match 39.7%; Score 46; DB 1; Length 859;
 Best Local Similarity 38.9%; Pred. No. 48;
 Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 18
 Qy 1 KENSAFPFFCCNDNVNT 18
 Db 28 EENTMFOQYCTTDSKNS 45

C; Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C; Accession: S07589
 R; McGuire, T.C.; Lacy, P.A.; O'Rourke, K.I.
 Nucleic Acids Res. 18, 196, 1990.
 A; Title: cDNA sequence of the env gene of a pathogenic equine infectious anemia lentivirus
 A; Reference number: S07589; MUID:90174929; PMID:2155398
 A; Accession: S07589
 A; Status: translation not shown
 A; Molecule type: genomic RNA
 A; Residues: 1-859 <MGI>
 A; Cross-references: UNIPROT:P16082; EMBL:X16388; NID:959246; PID:CAA34856.1; PID:959247
 C; Genetics:
 A; Gene: env
 C; Superfamily: equine infectious anemia virus env polyprotein
 C; Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F; 1-22/Domain: signal sequence #status predicted <SIG>
 F; 23-44/Domain: coat protein gp90 #status predicted <GP1>
 F; 75-93/Domain: transmembrane #status predicted <TM1>
 F; 145-859/Domain: coat protein gp45 #status predicted <GP2>
 F; 446-462/Domain: transmembrane #status predicted <TM2>
 F; 614-636/Domain: transmembrane #status predicted <TM3>
 F; 787-807/Domain: transmembrane #status predicted <TM4>
 F; 816-835/Domain: transmembrane #status predicted <TM5>
 F; 40,112,141,148,186,214,233,244,313,340,368,399,406,411,483,490,550,557,752/Binding site

| Query Match | Score | Length |
|--------------------|-------|--------------|
| Best Local Matches | 39.7% | 859 |
| Similarity | 38.9% | |
| Matches | 7; | Conservative |
| | 6; | Mismatches |
| | 5; | Indels |
| | 0; | Gaps |
| | 0; | |

Pred. No. 48;

Qy 1 KENSAFFPFCNDNVTNT 18
 :||: :|: |::|: :|:
 Db 28 EENTMRFQPYCYNNDSKNS 45

Search completed: February 5, 2005, 20:05:45
 Job time : 20.661 secs

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| Scoring table: | BLOSUM62 | | | | | |
|--|--|-------|--------|--------|--------------------------|-------------------------------------|
| Gapop: | 10.0 , Gapext 0.5 | | | | | |
| Searched: | 1612378 seqs, 512079187 residues | | | | | |
| Total number of hits satisfying chosen parameters: | 1612378 | | | | | |
| Minimum DB seq length: | 0 | | | | | |
| Maximum DB seq length: | 2000000000 | | | | | |
| Post-processing: | Minimum Match 0% Maximum Match 100% Listing first 45 summaries | | | | | |
| Database : | UniProt 03: 1: uniprot_sprot: 2: uniprot_trembl: * | | | | | |
| Pred. | No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution. and is derived by analysis of the total score distribution. | | | | | |
| SUMMARIES | | | | | | |
| Result No. | Query | Match | Length | DB | ID | Description |
| 1 | 165 | 100.0 | 241 | 1 | TSN1 HUMAN | 060635 homo sapien |
| 2 | 56 0 | 241 | 2 | Q6AYR9 | 06ayr9 rattus norvegicus | |
| 3 | 45.7 | 282 | 2 | Q86FC1 | Q86fc1 schistosoma | |
| 4 | 51 | 44.0 | 91 | 2 | Q6J758 | Q6j758 neurospora |
| 5 | 51 | 44.0 | 91 | 2 | Q6J763 | Q6j763 neurospora |
| 6 | 51 | 44.0 | 91 | 2 | Q6J766 | Q6j766 neurospora |
| 7 | 51 | 44.0 | 91 | 2 | Q6J767 | Q6j767 neurospora |
| 8 | 51 | 44.0 | 91 | 2 | Q6J768 | Q6j768 neurospora |
| 9 | 51 | 44.0 | 91 | 2 | Q6J769 | Q6j769 neurospora |
| 10 | 51 | 44.0 | 108 | 1 | RODL NEUCH | Q04571 neurospora |
| 11 | 51 | 44.0 | 860 | 1 | ENV_EIAVS | P22410 equine infestation |
| 12 | 51 | 44.0 | 863 | 2 | Q6AXF9 | Q6axf9 mus musculus |
| 13 | 51 | 44.0 | 923 | 2 | Q91X64 | Q91x64 mus musculus |
| 14 | 50 | 43.1 | 91 | 2 | Q6J765 | Q6j765 neurospora |
| 15 | 50 | 43.1 | 240 | 2 | Q99J59 | Q99j59 mus musculus |
| 16 | 50 | 43.1 | 301 | 1 | AMPB_STLSD | P95953 sulfolobus |
| 17 | 50 | 43.1 | 489 | 2 | Q651E0 | Q651e0 oryza sativa |
| 18 | 50 | 43.1 | 565 | 2 | Q97582 | Q97582 sus scrofa |
| 19 | 50 | 43.1 | 566 | 1 | EST1_PIG | Q29550 sus scrofa |
| 20 | 49.5 | 42.7 | 850 | 2 | Q700T4 | Q700t4 human immunodeficiency virus |
| 21 | 49 | 42.2 | 91 | 1 | NLT1_PRUDO | P82534 prunus domestica |
| 22 | 48 | 41.4 | 810 | 2 | Q6NBFT3 | Q6nbft3 rhodopeudo |
| 23 | 48 | 41.4 | 888 | 2 | Q9LST1 | Q9lst1 arabidopsis |
| 24 | 48 | 41.4 | 1293 | 1 | XPC_DROME | Q24535 drosophila |
| 25 | 48 | 41.4 | 1293 | 2 | Q9U3Z1 | Q9u3z1 drosophila |
| 26 | 48 | 41.4 | 1293 | 2 | Q9V7A8 | Q9v7a8 drosophila |
| 27 | 48 | 41.4 | 1294 | 2 | Q8MLA2 | Q8mla2 drosophila |
| 28 | 48 | 41.4 | 1623 | 2 | Q7PDV5 | Q7pdv5 plasmocitoma |
| 29 | 47 | 40.5 | 297 | 2 | Q6OWY8 | Q6owy8 equine infestation |
| 30 | 47 | 40.5 | 375 | 2 | Q8EH13 | Q8eh13 shewindlella |
| 31 | 46 | 39.7 | 397 | 2 | Q66747 | Q66747 equine infestation |

ALIGNMENTS

| | | |
|------------|--|--------------|
| RESULT 1 | TSN1 HUMAN STANDARD; | PRT; 241 AA. |
| ID | T-SN1 HUMAN STANDARD; | |
| AC | 060635 ; 060745 ; | |
| DT | 16-OCT-2001 (Rel. 40, Created) | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | |
| DB | Tetraspanin 1 (Tspan-1) (Tetraspan NET-1) (Tetraspanin TM4-C). | |
| GN | Name=TPSPAN1; | |
| OS | Homo sapiens (Human) | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; | |
| NCBI_TaxID | 9606; | |
| RN | SEQUENCE FROM N.A. | |
| RX | MEDLINE=98390278 ; PubMed=9714763 ; DOI=10.1016/S0167-4781(98)00087-6 ; | |
| RA | Todd S.C., Doctor V.S., Levy S. ; | |
| RT | "Sequences and expression of six new members of the tetraspanin/TM4SP family". | |
| RL | Biochim. Biophys. Acta 1399:101-104 (1998). | |
| RN | [1] | |
| RN | SEQUENCE FROM N.A. | |
| RA | Rubinstein E., Serru V., Boucheix C. ; | |
| RT | "New tetraspans identified in the EST database"; | |
| RL | Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases. | |
| RN | [3] | |
| RP | SEQUENCE FROM N.A. | |
| RA | Puls K.L., Ni J., Liu D., Morahan G., Wright M.D. ; | |
| RA | "The molecular characterization of four tetraspans in the family". | |
| RT | Biophys. Acta 1399:101-104 (1998). | |
| RL | [2] | |
| RN | SEQUENCE FROM N.A. | |
| RA | Rubinstein E., Serru V., Boucheix C. ; | |
| RT | "New tetraspans identified in the EST database"; | |
| RL | Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases. | |
| RN | [4] | |
| RP | SEQUENCE FROM N.A. | |
| RC | SEQUENCE=Col0. | |
| RX | MEDLINE=22388257 ; PubMed=12477932 ; DOI=10.1073/pnas.242603899 ; | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schueler C.M., Schulter G.D., Altchuler S.R., Zeeberg B., Buetow K.H., Scheaffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong J., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Yoshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutard G.G., Blakesley R.W., Touchman J.W., Dickson M.C., Rodriguez A.C., Grimes J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.B., Scherch A., Schein J.E., Jones S.J.M., Marra M.A. ; | |
| RA | "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences". | |
| RT | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). | |

| | | |
|--|---|---|
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable). | RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McCowan P.J., McErlean K.J., Malek J.A., Guaratne P.H., Bosak S.A., McGowan P.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Sodergren E.J., Villeneuve D.K., Muzny D.M., Madan A., Rodriques S., Sanchez A., Viallette D.K., Helton E., Kettman M., Madan A., Rodriguez Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J.W., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnier A., Schein J.E., Jones S.J., Marr M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). |
| CC | -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family. | RN [2]. |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). | RN RP SEQUENCE FROM N.A. |
| CC | DR EMBL; AF054838; AAC69714.1; . | RC TISSUE=Kidney; |
| CC | DR EMBL; AF065388; AAC17119.1; . | RA Director MGC Project; |
| CC | DR EMBL; BC07230; AAH07290.1; . | RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases. |
| CC | DR EMBL; ARF08364.1; . | DR EMBL; BC078938; AAH08938.1; . |
| CC | DR PIR; A59262; A59262.1; . | GO; GO:0016021; C:Integral to membrane; IEA. |
| CC | DR InvDB; HIX000543; . | DR InterPro; IPR02229; RhesusRHD. |
| CC | DR GO; GO:0016021; C:integral to membrane; TAS. | DR InterPro; IPR00952; Tetraspanin. |
| CC | DR InterPro; IPR00321; Transmembrane. | DR Pfam; PF00335; Tetraspanin_1. |
| CC | DR InterPro; IPR00321; Transmembrane_4. | DR PRINTS; PRO0342; RHESUSRHD. |
| CC | DR InterPro; PR00335; Tetraspanin; 1. | DR PROSITE; PS00421; TM4_1; 1. |
| CC | DR InterPro; PR00259; TMFOUR. | SQ SEQUENCE 241 AA; 26453 MW; 9118B86546D1A70 CRC64; |
| CC | DR Prints; PS00421; TM4_1; FALSE_NEG. | Query Match 56.0%; Score 65; DB 2; Length 241; |
| CC | KW Glycoprotein; Transmembrane. | Best Local Similarity 71.4%; Pred. No. 0.043; 1; Mismatches 10; Conservative 3; Indels 0; Gaps 0; |
| FT DOMAIN 1 11 Cytoplasmic (Potential). FT DOMAIN 1 11 Cytoplasmic (Potential). | Matches 165 KENKVFPPFCANN 178 | |
| FT DOMAIN 12 32 Extracellular (Potential). FT DOMAIN 12 32 Extracellular (Potential). | Qy 1 KENSAFPFPCCNDN 14 | |
| FT DOMAIN 33 52 Potential. FT DOMAIN 33 52 Potential. | Db 165 KENKVFPPFCANN 178 | |
| FT DOMAIN 53 73 Cytoplasmic (Potential). FT DOMAIN 74 88 Cytoplasmic (Potential). | | |
| FT DOMAIN 74 88 Potential. FT DOMAIN 89 109 Potential. | | |
| FT DOMAIN 89 109 Extracellular (Potential). FT DOMAIN 110 211 Extracellular (Potential). | | |
| FT DOMAIN 110 211 Potential. FT DOMAIN 212 232 Cytoplasmic (Potential). | | |
| FT DOMAIN 233 241 N-linked (GlcNAc. .) (Potential). FT DOMAIN 141 141 N-linked (GlcNAc. .) (Potential). | | |
| FT CARBOHYD 141 141 N-linked (GlcNAc. .) (Potential). FT CARBOHYD 154 154 N-linked (GlcNAc. .) (Potential). | | |
| FT CARBOHYD 154 154 N-linked (GlcNAc. .) (Potential). FT CARBOHYD 178 178 N-linked (GlcNAc. .) (Potential). | | |
| FT CARBOHYD 178 178 N-linked (GlcNAc. .) (Potential). FT CARBOHYD 184 184 N-linked (GlcNAc. .) (Potential). | | |
| FT CONFLICT 189 189 K > E (in Ref. 1). FT CONFLICT 189 189 K > E (in Ref. 1). | | |
| SQ SEQUENCE 241 AA; 26301 MW; AF938AB7147/CB884 CRC64; RESULT 3 Q86FC1 PRELIMINARY; PRT; 282 AA. | | |
| Query Match 100.0%: Score 116; DB 1; Length 241; Best Local Similarity 100.0%; Pred. No. 3.8e-10; Indels 0; Gaps 0; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | AC Q86FC1 ID Q86FC1 PRELIMINARY; PRT; 282 AA. | |
| Qy 1 KENSAFPFPCCNDNTNTAN 20 Db 165 KENSAFPFPCCNDNTNTAN 184 | DT DT 01-JUN-2003 (TRMBLrel). 24; Created | |
| DE DE Clone ZZD391. mRNA sequence. | DT DT 01-MAR-2004 (TRMBLrel). 26; Last annotation update | |
| OS OS Schistosoma japonicum (Blood fluke). | DE DE Schistosoma japonicum (Blood fluke). | |
| OC OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidaida; Schistosomatidae; Schistosomatida; Schistosoma. | OC OC Schistosomatidae; Schistosomatida; Schistosoma. | |
| OX OX NCBI_TAXID=6182; NCBI_TAXID=6182; [1] | OX OX NCBI_TAXID=6182; [1] | |
| RN RN RP SEQUENCE FROM N.A. | RN RN SEQUENCE FROM N.A. | |
| RX RX PMID=22879925; PubMed=12973349; DOI=10.1038/ng1236; DT DT 01-JUN-2003 (TRMBLrel). 24; Last sequence update | RX RX PMID=22879925; PubMed=12973349; DOI=10.1038/ng1236; DT DT 01-JUN-2003 (TRMBLrel). 24; Last sequence update | |
| RA RA Hu W., Yan Q., Shen D.K., Liu F., Song R.D., Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brinley P.J., McManus D.P., Xie C.L., Fang Z., Chen Z., Han Z.G.; "Evolutionary and biomedical implications of a Schistosoma japonicum DNA resource"; RT RT Complementary DNA resource"; DR DR EMBL; AY222942; AAP05554.1; - | RA RA Hu W., Yan Q., Shen D.K., Liu F., Song R.D., Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brinley P.J., McManus D.P., Xie C.L., Fang Z., Chen Z., Han Z.G.; "Evolutionary and biomedical implications of a Schistosoma japonicum DNA resource"; RT RT Complementary DNA resource"; DR DR EMBL; AY222942; AAP05554.1; - | |
| RA RA SEQUENCE FROM N.A. | DR DR PFM; PF00315; Tetraspanin_1. | |
| RX RX Published=12477932; DOI=10.1073/pnas.242603899; DT DT 01-JUN-2003 (TRMBLrel). 28; Last annotation update | SQ SEQUENCE 282 AA; 31153 MW; 6CBB4D2ED2B37C4 CRC64; | |
| RA RA Straubberg R.L., Feingold E.A., Grouse L.H., George J.G., Klaunher R.D., Collins F.S., Wagner L., Shearman C.M., Schuler G.D., Altshull S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., RA RA SEQUENCE 282 AA; 31153 MW; 6CBB4D2ED2B37C4 CRC64; | Query Match 45.7%; Score 53; DB 2; Length 282; Best Local Similarity 66.7%; Pred. No. 3.9%; Matches 8; Conservative 3; Indels 0; Gaps 0; | |
| RA RA SEQUENCE FROM N.A. | Qy 3 NSAFPPFCNDN 14 | |

| Db | 198 NSKYPFCKFN 209 | Matches | .8; Conservative | 1; Mismatches | 2; Indels | 0; Gaps | 0; |
|---|---|--------------------------|------------------|---------------|-----------|---------|----|
| RESULT 4 | | | | | | | |
| Q6J758 | PRELIMINARY; | PRT; | 91 AA. | | | | |
| ID Q6J758 | | | | | | | |
| AC | | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Created) | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Last sequence update) | | | | | | |
| DT 25-Oct-2004 | (TREMBLrel. 28; Last annotation update) | | | | | | |
| DB Easily wettable (Fragment). | | | | | | | |
| OS Neurospora itrophila. | | | | | | | |
| OC Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | | | | | | |
| OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. | | | | | | | |
| OX NCBI_TaxID:40126; | | | | | | | |
| RN [1] | | | | | | | |
| RP SEQUENCE FROM N.A. | | | | | | | |
| RC STRAIN=P8085; | | | | | | | |
| RA Winefield R.D., Beever R.E., Newcomb R.D., Haverkamp R.G., | | | | | | | |
| RA Templeton M.D.; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. | | | | | | | |
| DR EMBL; AY577557; ATAT9533_1; -. | | | | | | | |
| DR EMBL; AY577550; ATAT0751_1; -. | | | | | | | |
| DR GO; GO:0005618; C:cell wall; IBA. | | | | | | | |
| DR GO; GO:0005199; F:structural constituent of cell wall; IEA. | | | | | | | |
| DR InterPro; IPR001338; Hydrophobin. | | | | | | | |
| DR Pfam; PF01185; Hydrophobin; 1. | | | | | | | |
| DR SMART; SM00075; HYDRO; 1. | | | | | | | |
| DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1. | | | | | | | |
| PT NON-TER 1 1 | | | | | | | |
| PT NON-TER 91 91 | SEQUENCE 91 AA; 9095 MW; | EE02886C772C0220 CRC64; | | | | | |
| Query Match Score 51; DB 2; Length 91; | | | | | | | |
| Best Local Similarity 72.7%; Pred. No. 2.5; | | | | | | | |
| Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0; | | | | | | | |
| Qy 10 CCNDVNTAN 20 | | | | | | | |
| Db 77 CCKDDVNTGN 87 | | | | | | | |
| RESULT 5 | | | | | | | |
| Q6J763 | PRELIMINARY; | PRT; | 91 AA. | | | | |
| ID Q6J763 | | | | | | | |
| AC Q6J763; | | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Created) | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Last sequence update) | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Last annotation update) | | | | | | |
| DB Easily wettable (Fragment). | | | | | | | |
| OS Neurospora discreta. | | | | | | | |
| OC Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | | | | | | |
| OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. | | | | | | | |
| OX NCBI_TaxID:29819; | | | | | | | |
| RN [1] | | | | | | | |
| RP SEQUENCE FROM N.A. | | | | | | | |
| RC STRAIN=Kirbyville-6; | | | | | | | |
| RA Winefield R.D., Beever R.E., Newcomb R.D., Haverkamp R.G., | | | | | | | |
| RA Templeton M.D.; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. | | | | | | | |
| DR EMBL; AY577551; ATAT0752_1; -. | | | | | | | |
| DR GO; GO:0005618; C:cell wall; IBA. | | | | | | | |
| DR GO; GO:0005199; F:structural constituent of cell wall; IEA. | | | | | | | |
| DR InterPro; IPR001338; Hydrophobin. | | | | | | | |
| DR Pfam; PF01185; Hydrophobin; 1. | | | | | | | |
| DR SMART; SM00075; HYDRO; 1. | | | | | | | |
| DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1. | | | | | | | |
| PT NON-TER 1 1 | | | | | | | |
| PT NON-TER 91 91 | SEQUENCE 91 AA; 9076 MW; | 1761089907CB8FFEA CRC64; | | | | | |
| Query Match Score 51; DB 2; Length 91; | | | | | | | |
| Best Local Similarity 72.7%; Pred. No. 2.5; | | | | | | | |
| Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0; | | | | | | | |
| Qy 10 CCNDVNTAN 20 | | | | | | | |
| Db 77 CCKDDVNTGN 87 | | | | | | | |
| RESULT 6 | | | | | | | |
| Q6J766 | PRELIMINARY; | PRT; | 91 AA. | | | | |
| ID Q6J766 | | | | | | | |
| AC Q6J766; | | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Created) | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Last sequence update) | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Last annotation update) | | | | | | |
| DB Easily wettable (Fragment). | | | | | | | |
| OS Neurospora tetrasperma. | | | | | | | |
| OC Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | | | | | | |
| OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. | | | | | | | |
| OX NCBI_TaxID=40127; | | | | | | | |
| RN [1] | | | | | | | |
| RP SEQUENCE FROM N.A. | | | | | | | |
| RC STRAIN=85A; | | | | | | | |
| RA Winefield R.D., Beever R.E., Newcomb R.D., Haverkamp R.G., | | | | | | | |
| RA Templeton M.D.; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. | | | | | | | |
| DR EMBL; AY577548; ATAT0749_1; -. | | | | | | | |
| DR GO; GO:0005199; F:structural constituent of cell wall; IEA. | | | | | | | |
| DR InterPro; IPR001338; Hydrophobin. | | | | | | | |
| DR Pfam; PF01185; Hydrophobin; 1. | | | | | | | |
| DR SMART; SM00075; HYDRO; 1. | | | | | | | |
| DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1. | | | | | | | |
| PT NON-TER 1 1 | | | | | | | |
| PT NON-TER 91 91 | SEQUENCE 91 AA; 9063 MW; | ODDBA76CD8460EA CRC64; | | | | | |
| Query Match Score 51; DB 2; Length 91; | | | | | | | |
| Best Local Similarity 72.7%; Pred. No. 2.5; | | | | | | | |
| Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0; | | | | | | | |
| Qy 10 CCNDVNTAN 20 | | | | | | | |
| Db 77 CCKDDVNTGN 87 | | | | | | | |
| RESULT 7 | | | | | | | |
| Q6J767 | PRELIMINARY; | PRT; | 91 AA. | | | | |
| ID Q6J767 | | | | | | | |
| AC Q6J767; | | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Created) | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Last sequence update) | | | | | | |
| DT 05-JUL-2004 | (TREMBLrel. 27; Last annotation update) | | | | | | |
| DB Easily wettable (Fragment). | | | | | | | |
| OS Neurospora panonica. | | | | | | | |
| OC Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | | | | | | |
| OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. | | | | | | | |
| OX NCBI_TaxID=85778; | | | | | | | |
| RN [1] | | | | | | | |
| RP SEQUENCE FROM N.A. | | | | | | | |
| RC STRAIN=TRTC 51327; | | | | | | | |
| RA Winefield R.D., Beever R.E., Newcomb R.D., Haverkamp R.G., | | | | | | | |
| RA Templeton M.D.; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. | | | | | | | |
| DR EMBL; AY577547; ATAT0748_1; -. | | | | | | | |
| DR GO; GO:0005199; C:cell wall; IEA. | | | | | | | |
| DR InterPro; IPR001338; Hydrophobin. | | | | | | | |
| DR Pfam; PF01185; Hydrophobin; 1. | | | | | | | |
| DR SMART; SM00075; HYDRO; 1. | | | | | | | |
| DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1. | | | | | | | |
| PT NON-TER 1 1 | | | | | | | |
| PT NON-TER 91 91 | SEQUENCE 91 AA; 9063 MW; | ODDBA76CD8460EA CRC64; | | | | | |
| Query Match Score 51; DB 2; Length 91; | | | | | | | |
| Best Local Similarity 72.7%; Pred. No. 2.5; | | | | | | | |
| Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0; | | | | | | | |
| Qy 10 CCNDVNTAN 20 | | | | | | | |
| Db 77 CCKDDVNTGN 87 | | | | | | | |

reproductive structures, dispersal of aerial spores and adhesion of pathogens to host structures. Important for the formation of hydrophobic rodlet layers of asexually-produced spores.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DEVELOPMENTAL STAGE: Accumulates during conidiation but not during germination.

CC -!- INDUCTION: Expression is controlled by blue light and by a circadian clock. Also induced by glucose, nitrogen and carbon starvation.

CC -!- SIMILARITY: Belongs to the fungal hydrophobin family.

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DR EMBL; X67339; CAA47754_1; -
 EMBL; X62170; CAA44101_1; -
 DR PIR; A46222; A46222.
 DR InterPro; IPR001338; Hydrophobin.
 PFam; PF01185; Hydrophobin; 1.
 SMART; SM00075; HYDRO; 1.
 PROSITE; PS00596; HYDROPHOBIN; 1.
 DR SIGNAL; 1 26 Potential.
 PT CHAIN 27 108 Hydrophobin.
 SQ SEQUENCE 108 AA; 10875 MW; 7BB5992A9C173E9 CRC64;
 Query Match Score 51; DB 1; Length 108;
 Best Local Similarity 72.7%; Pred. No. 3;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 10 CCNDNTNTAN 20
 Db 86 CCKDDDTNTGN 96

RESULT 11
 ENV_EIAV5 STANDARD; PRT; 860 AA.
 AC P22430;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE ENV polyprotein precursor (Coat polypeptide) [Contains: Coat protein GP90; Coat protein GP45].
 GN Name=ENV;
 OS Equine infectious anemia virus (clone P3.2-5) (EIAV).
 OC Viruses; Retroviridae; Lentiviruses.

NCBI_TaxID=11669;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=2825406;
 RA Payne S.L., Fang F.D., Liu C.P., Dhruba B.R., Rwanbo P., Issel C.J.,
 Montelaro R.C.;
 RT "Antigenic variation and lentivirus persistence: variations in envelope gene sequences during EIAV infection resemble changes reported for sequential isolates of HIV.";
 RT Virology 161:31-31(1987).

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DR EMBL; M18388; AAA66410_1; -

| | |
|--|--|
| CC | PIR; D34027; VCLJJE4. |
| CC | DR InterPro; IPR01027; Gp45_EIAV. |
| CC | DR InterPro; IPR01361; Gp10_EIAV. |
| CC | DR Pfam; PF01045; EIAV_Gp45_1. |
| CC | DR Pfam; PF00971; EIAV_Gp90_1. |
| CC | KW Coat Protein; Glycoprotein; Polypeptide; Signal; Transmembrane. |
| CC | POTENTIAL. |
| FT SIGNAL 1 22 | |
| FT CHAIN 23 860 | |
| FT CHAIN 23 445 | |
| FT CHAIN 23 860 | Env Polyprotein. |
| FT CHAIN 23 445 | Coat Protein GP90. |
| FT CHAIN 23 860 | Coat Protein GP45. |
| FT TRANSMEM 75 93 | Potential. |
| FT TRANSMEM 447 463 | Potential. |
| FT TRANSMEM 615 637 | Potential. |
| FT TRANSMEM 798 808 | Potential. |
| FT TRANSMEM 817 836 | Potential. |
| FT CAREOHYD 40 40 | (Potential). |
| FT CAREOHYD 112 112 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 141 141 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 148 148 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 186 186 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 201 201 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 214 214 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 235 235 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 244 244 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 308 308 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 337 337 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 340 340 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 346 346 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 369 369 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 400 400 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 407 407 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 412 412 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 423 423 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 484 484 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 491 491 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 551 551 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 558 558 | N-Linked (GlcNAc. . .) |
| FT CAREOHYD 753 753 | N-Linked (GlcNAc. . .) |
| SQ SEQUENCE 860 AA; 97020 MW; 0037EB61528E0DD CRC64; | (Potential). |
| Query Match Score 51; DB 1; Length 860; | |
| Best Local Similarity 44.0%; Pred. No. 3; | |
| Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0; | |
| Qy 1 KENSAFPPFCNDNTNT 18 | |
| Db 28 EENTIFQOPICYNNNNKSNS 45 | |
| RESULT 12 | |
| Q6AXF9 PRELIMINARY; PRT; 863 AA. | |
| ID Q6AXF9 | |
| AC Q6AXF9; | |
| DT 25-OCT-2004 (TREMBrel. 28, Created) | |
| DT 25-OCT-2004 (TREMBrel. 28, Last sequence update) | |
| DB 28 EENTIFQOPICYNNNNKSNS 45 | |
| DE Seq12 protein. | |
| GN Name=Se612; | |
| OS Mus musculus (Mouse). | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; | |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | |
| OX NCBI_TaxID=10900; | |
| RN [1] | |
| RP SEQUENCE FROM N.A. | |
| RC STRAIN=C57BL/6; TISSUE=Brain; | |
| RX PubRef=1247932; DOI=10.1073/pnas.242603899; | |
| RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenkin C.M., Schuler G.D., Altchule S.F., Zeeberg B.B., Buetow K.H., Scheaffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiach F., Diatchenko L., Maruskin K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C., | |

- DR GO; GO:0016021; C: integral membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR Pfam; PF00431; CUB; 2.
 DR SMART; SM00032; Sushi; 5.
 DR SMART; SM00042; CCP; 5.
 DR PROSITE; PS01189; CUB; 3.
 DR PROSITE; PS050923; SUSHI; 5.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 923 AA; 99077 MW; DD15ADF50848889 CRC64;
- Query Match 44.0%; Score 51; DB 2; Length 923;
 Best Local Similarity 50.0%; Pred. No. 28;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
- Qy 1 KENSAFPFCCNDNVNT 18
 :|||:|||:|||:
 Db 460 EEDRCFPFLAHGNVTTT 477
- RESULT 14
 ID Q6J765 PRELIMINARY; PRT; 91 AA.
 AC Q6J765; PRT; 91 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DB Easily wettable (Fragment).
 OS Neurospora tetraspora.
 OC Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OX NCBI_TaxID=40127.
 RN SEQUENCE FROM N.A.
 RC STRAIN=CB5 259 35;
 RA Winefield R.D., Beever R.E., Newcomb R.D., Haverkamp R.G.,
 RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL;AY577549; ATAT0750_1; -
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0005199; F:structural constituent of cell wall; IEA.
 DR InterPro; IPR01338; Hydrophobin.
 DR SMART; SM00075; HYDRO; 1.
 DR PROSITE; PS000936; HYDROPHOBIN; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 91 91
 SQ SEQUENCE 91 AA; 9005 MW; ODDB4A36D8460BA CRC64;
- Query Match 43.1%; Score 50; DB 2; Length 91;
 Best Local Similarity 72.7%; Pred. No. 3.7%;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
- RESULT 15
 ID Q99059 PRELIMINARY; PRT; 240 AA.
 AC Q99059; PRT; 240 AA.
 DT 01-TUN-2001 (TREMBLrel. 17, Created)
 DT 01-TUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE RIKEN cDNA 9030418M05 (Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030418M05 product:similar to tetraspan TSPAN-11, Name=9030418M05Rik; Mus musculus (Mouse)).
 DE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
- [1] RN RP SEQUENCE FROM N.A.
 RC STRAIN=NMRJ; TISSUE=Mammary tumor;
 RX MEDLINE=22388237; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klaunzer R.D., Peingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshikawa S., Carnicci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., FAHEY J., Hellon E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.J., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J., Marr A.M.; "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences,"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
- [2] RN RP SEQUENCE FROM N.A.
 RC STRAIN=NMRJ; TISSUE=Mammary tumor;
 RA Strausberg R.; Subramanian (FEB-2001) to the EMBL/GenBank/DBJ databases.
- [3] RN RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Colon; MEDLINE=927953; PubMed=10496336; DOI=10.1016/S0076-6879(99)03004-9; RA Carnicci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning,"; RT Meth. Enzymol. 303:19-44 (1999).
- [4] RN RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Colon; MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500; RA RIKEN FANTOM Consortium; RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690 (2001).
- [5] RN RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Colon; MEDLINE=927953; PubMed=10496336; DOI=10.1016/S0076-6879(99)03004-9; RA Carnicci P., Hayashizaki Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Nature 420:553-573 (2002).
- [6] RN RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Colon; MEDLINE=20530913; PubMed=11042159; DOI=10.1101/gr.145100; RA The RIKEN Genome Exploration Research Group Phase I & II Team; RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwara S., Inoue K., Ishikawa T., Tanaka T., Ohara E., Watabiki M., Yoneda Y., Ishikawa T., Ozawa K., Matsuda S., Kawai J., Okazaki Y., Muranatsu M., Inoue Y., Kira A., Hayashi Y.; RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.,"; RT

RL Genome Res. 10:1757-1771 (2000).
 RN [8]
 RP SEQUENCE FROM N_A.
 RC STRAIN=C57Bl/6J; TISSUE=Colon;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoaka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kuribara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numasaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shiba Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamoto T., Yamamoto T., Yasunishi A.,
 RA Yoshiida K., Yoshiino M., Muramatsu M., Hayashizaki Y.,
 RL Submitted (APR-2002) to the EMBL/Genbank/DDBJ databases.
 DR EMBL; BC03448; AAH03448.1;
 DR EMBL; AK078869; BAC37431.1;
 DR EMBL; MGTR1914055; 9030418M05Rik.
 DR GO:0005615; C:extracellular space; TAS.
 DR GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR002229; RhesusRHD.
 DR InterPro; IPR008352; Tetraspanin.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; Tetraspanin_1.
 DR PRINTS; PR00342; RHESUSRHD.
 DR PROSITE; PS00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 SQ SEQUENCE 240 AA; 26356 MW; AD4C448A32BC2999 CRC64;
 Query Match 43.1%; Score 50; DB 2; Length 240;
 Best Local Similarity 72.7%; Pred. No. 9, 3;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 KENSAFPPCC 11
 Db 165 KENKVFPCC 175

Search completed: February 5, 2005, 20:04:44
 Job time : 96.9153 secs